



SEQUENCE LISTING

<110> Gorman, Daniel M.

<120> MAMMALIAN RECEPTOR PROTEINS; RELATED REAGENTS AND METHODS

<130> DX01170K

<140> 09/863,818

<141> 2001-05-23

<150> US 60/206,862

<151> 2000-05-24

<160> 22

<170> PatentIn version 3.1

<210> 1

<211> 1796

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (4)..(1509)

<223>

<220>

<221> mat_peptide

<222> (46)..()

<223>

<400> 1

gcg	atg	tcg	ctc	gtg	ctg	cta	agc	ctg	gcc	gcg	ctg	tgc	agg	agc	gcc	48
Met	Ser	Leu	Val	Leu	Leu	Ser	Leu	Ala	Ala	Leu	Cys	Arg	Ser	Ala		
				-10					-5				-1	1		

gta	ccc	cga	gag	ccg	acc	gtt	caa	tgt	ggc	tct	gaa	act	ggg	cca	tct	96
Val	Pro	Arg	Glu	Pro	Thr	Val	Gln	Cys	Gly	Ser	Glu	Thr	Gly	Pro	Ser	
			5					10					15			

cca	gag	tgg	atg	cta	caa	cat	gat	cta	atc	ccg	gga	gac	ttg	agg	gac	144
Pro	Glu	Trp	Met	Leu	Gln	His	Asp	Leu	Ile	Pro	Gly	Asp	Leu	Arg	Asp	
		20					25					30				

ctc	cga	gta	gaa	cct	gtt	aca	act	agt	gtt	gca	aca	ggg	gac	tat	tca	192
Leu	Arg	Val	Glu	Pro	Val	Thr	Thr	Ser	Val	Ala	Thr	Gly	Asp	Tyr	Ser	
		35				40					45					

att	ttg	atg	aat	gta	agc	tgg	gta	ctc	cgg	gca	gat	gcc	agc	atc	cgc	240
Ile	Leu	Met	Asn	Val	Ser	Trp	Val	Leu	Arg	Ala	Asp	Ala	Ser	Ile	Arg	
		50			55				60					65		

ttg	ttg	aag	gcc	acc	aag	att	tgt	gtg	acg	ggc	aaa	agc	aac	ttc	cag	288
Leu	Leu	Lys	Ala	Thr	Lys	Ile	Cys	Val	Thr	Gly	Lys	Ser	Asn	Phe	Gln	
				70					75					80		

tcc	tac	agc	tgt	gtg	agg	tgc	aat	tac	aca	gag	gcc	ttc	cag	act	cag	336
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

Ser	Tyr	Ser	Cys	Val	Arg	Cys	Asn	Tyr	Thr	Glu	Ala	Phe	Gln	Thr	Gln	
			85				90						95			
acc	aga	ccc	tct	ggt	ggt	aaa	tgg	aca	ttt	tcc	tat	atc	ggc	ttc	cct	384
Thr	Arg	Pro	Ser	Gly	Gly	Lys	Trp	Thr	Phe	Ser	Tyr	Ile	Gly	Phe	Pro	
		100					105					110				
gta	gag	ctg	aac	aca	gtc	tat	ttc	att	ggg	gcc	cat	aat	att	cct	aat	432
Val	Glu	Leu	Asn	Thr	Val	Tyr	Phe	Ile	Gly	Ala	His	Asn	Ile	Pro	Asn	
	115					120					125					
gca	aat	atg	aat	gaa	gat	ggc	cct	tcc	atg	tct	gtg	aat	ttc	acc	tca	480
Ala	Asn	Met	Asn	Glu	Asp	Gly	Pro	Ser	Met	Ser	Val	Asn	Phe	Thr	Ser	
130					135					140					145	
cca	ggc	tgc	cta	gac	cac	ata	atg	aaa	tat	aaa	aaa	aag	tgt	gtc	aag	528
Pro	Gly	Cys	Leu	Asp	His	Ile	Met	Lys	Tyr	Lys	Lys	Lys	Cys	Val	Lys	
				150					155					160		
gcc	gga	agc	ctg	tgg	gat	ccg	aac	atc	act	gct	tgt	aag	aag	aat	gag	576
Ala	Gly	Ser	Leu	Trp	Asp	Pro	Asn	Ile	Thr	Ala	Cys	Lys	Lys	Asn	Glu	
			165				170						175			
gag	aca	gta	gaa	gtg	aac	ttc	aca	acc	act	ccc	ctg	gga	aac	aga	tac	624
Glu	Thr	Val	Glu	Val	Asn	Phe	Thr	Thr	Thr	Pro	Leu	Gly	Asn	Arg	Tyr	
		180					185					190				
atg	gct	ctt	atc	caa	cac	agc	act	atc	atc	ggg	ttt	tct	cag	gtg	ttt	672
Met	Ala	Leu	Ile	Gln	His	Ser	Thr	Ile	Ile	Gly	Phe	Ser	Gln	Val	Phe	
	195					200					205					
gag	cca	cac	cag	aag	aaa	caa	acg	cga	gct	tca	gtg	gtg	att	cca	gtg	720
Glu	Pro	His	Gln	Lys	Lys	Gln	Thr	Arg	Ala	Ser	Val	Val	Ile	Pro	Val	
210					215					220					225	
act	ggg	gat	agt	gaa	ggt	gct	acg	gtg	cag	ctg	act	cca	tat	ttt	cct	768
Thr	Gly	Asp	Ser	Glu	Gly	Ala	Thr	Val	Gln	Leu	Thr	Pro	Tyr	Phe	Pro	
				230					235					240		
act	tgt	ggc	agc	gac	tgc	atc	cga	cat	aaa	gga	aca	gtt	gtg	ctc	tgc	816
Thr	Cys	Gly	Ser	Asp	Cys	Ile	Arg	His	Lys	Gly	Thr	Val	Val	Leu	Cys	
			245					250					255			
cca	caa	aca	ggc	gtc	cct	ttc	cct	ctg	gat	aac	aac	aaa	agc	aag	ccg	864
Pro	Gln	Thr	Gly	Val	Pro	Phe	Pro	Leu	Asp	Asn	Asn	Lys	Ser	Lys	Pro	
		260					265					270				
gga	ggc	tgg	ctg	cct	ctc	ctc	ctg	ctg	tct	ctg	ctg	gtg	gcc	aca	tgg	912
Gly	Gly	Trp	Leu	Pro	Leu	Leu	Leu	Leu	Ser	Leu	Leu	Val	Ala	Thr	Trp	
	275					280					285					
gtg	ctg	gtg	gca	ggg	atc	tat	cta	atg	tgg	agg	cac	gaa	agg	atc	aag	960
Val	Leu	Val	Ala	Gly	Ile	Tyr	Leu	Met	Trp	Arg	His	Glu	Arg	Ile	Lys	
290					295				300						305	
aag	act	tcc	ttt	tct	acc	acc	aca	cta	ctg	ccc	ccc	att	aag	gtt	ctt	1008
Lys	Thr	Ser	Phe	Ser	Thr	Thr	Thr	Leu	Leu	Pro	Pro	Ile	Lys	Val	Leu	
				310					315					320		
gtg	gtt	tac	cca	tct	gaa	ata	tgt	ttc	cat	cac	aca	att	tgt	tac	ttc	1056
Val	Val	Tyr	Pro	Ser	Glu	Ile	Cys	Phe	His	His	Thr	Ile	Cys	Tyr	Phe	

325	330	335	
act gaa ttt ctt caa aac cat tgc aga agt gag gtc atc ctt gaa aag			1104
Thr Glu Phe Leu Gln Asn His Cys Arg Ser Glu Val Ile Leu Glu Lys			
340	345	350	
tgg cag aaa aag aaa ata gca gag atg ggt cca gtg cag tgg ctt gcc			1152
Trp Gln Lys Lys Lys Ile Ala Glu Met Gly Pro Val Gln Trp Leu Ala			
355	360	365	
act caa aag aag gca gca gac aaa gtc gtc ttc ctt ctt tcc aat gac			1200
Thr Gln Lys Lys Ala Ala Asp Lys Val Val Phe Leu Leu Ser Asn Asp			
370	375	380	385
gtc aac agt gtg tgc gat ggt acc tgt ggc aag agc gag ggc agt ccc			1248
Val Asn Ser Val Cys Asp Gly Thr Cys Gly Lys Ser Glu Gly Ser Pro			
390	395	400	
agt gag aac tct caa gac ctc ttc ccc ctt gcc ttt aac ctt ttc tgc			1296
Ser Glu Asn Ser Gln Asp Leu Phe Pro Leu Ala Phe Asn Leu Phe Cys			
405	410	415	
agt gat cta aga agc cag att cat ctg cac aaa tac gtg gtg gtc tac			1344
Ser Asp Leu Arg Ser Gln Ile His Leu His Lys Tyr Val Val Val Tyr			
420	425	430	
ttt aga gag att gat aca aaa gac gat tac aat gct ctc agt gtc tgc			1392
Phe Arg Glu Ile Asp Thr Lys Asp Asp Tyr Asn Ala Leu Ser Val Cys			
435	440	445	
ccc aag tac cac ctc atg aag gat gcc act gct ttc tgt gca gaa ctt			1440
Pro Lys Tyr His Leu Met Lys Asp Ala Thr Ala Phe Cys Ala Glu Leu			
450	455	460	465
ctc cat gtc aag cag cag gtg tca gca gga aaa aga tca caa gcc tgc			1488
Leu His Val Lys Gln Gln Val Ser Ala Gly Lys Arg Ser Gln Ala Cys			
470	475	480	
cac gat ggc tgc tgc tcc ttg tagccaccc atgagaagca agagacctta			1539
His Asp Gly Cys Cys Ser Leu			
485			
aaggcttctt atcccaccaa ttacagggaa aaaacgtgtg atgacctga agcttactat			1599
gcagcctaca aacagcctta gtaattaaaa cattttatac caataaaaatt ttcaaatt			1659
gctaactaat gtagcattaa ctaacgattg gaaactacat ttacaacttc aaagctgttt			1719
tatacataga aatcaattac agctttaatt gaaaactgta accattttga taatgcaaca			1779
ataaagcatc ttcagcc			1796

<210> 2
 <211> 502
 <212> PRT
 <213> Homo sapiens
 <400> 2

Met Ser Leu Val Leu Leu Ser Leu Ala Ala Leu Cys Arg Ser Ala Val

-10

-5

-1 1

Pro Arg Glu Pro Thr Val Gln Cys Gly Ser Glu Thr Gly Pro Ser Pro
5 10 15

Glu Trp Met Leu Gln His Asp Leu Ile Pro Gly Asp Leu Arg Asp Leu
20 25 30

Arg Val Glu Pro Val Thr Thr Ser Val Ala Thr Gly Asp Tyr Ser Ile
35 40 45 50

Leu Met Asn Val Ser Trp Val Leu Arg Ala Asp Ala Ser Ile Arg Leu
55 60 65

Leu Lys Ala Thr Lys Ile Cys Val Thr Gly Lys Ser Asn Phe Gln Ser
70 75 80

Tyr Ser Cys Val Arg Cys Asn Tyr Thr Glu Ala Phe Gln Thr Gln Thr
85 90 95

Arg Pro Ser Gly Gly Lys Trp Thr Phe Ser Tyr Ile Gly Phe Pro Val
100 105 110

Glu Leu Asn Thr Val Tyr Phe Ile Gly Ala His Asn Ile Pro Asn Ala
115 120 125 130

Asn Met Asn Glu Asp Gly Pro Ser Met Ser Val Asn Phe Thr Ser Pro
135 140 145

Gly Cys Leu Asp His Ile Met Lys Tyr Lys Lys Lys Cys Val Lys Ala
150 155 160

Gly Ser Leu Trp Asp Pro Asn Ile Thr Ala Cys Lys Lys Asn Glu Glu
165 170 175

Thr Val Glu Val Asn Phe Thr Thr Thr Pro Leu Gly Asn Arg Tyr Met
180 185 190

Ala Leu Ile Gln His Ser Thr Ile Ile Gly Phe Ser Gln Val Phe Glu
195 200 205 210

Pro His Gln Lys Lys Gln Thr Arg Ala Ser Val Val Ile Pro Val Thr
215 220 225

Gly Asp Ser Glu Gly Ala Thr Val Gln Leu Thr Pro Tyr Phe Pro Thr
230 235 240

Cys Gly Ser Asp Cys Ile Arg His Lys Gly Thr Val Val Leu Cys Pro
245 250 255

Gln Thr Gly Val Pro Phe Pro Leu Asp Asn Asn Lys Ser Lys Pro Gly
260 265 270

Gly Trp Leu Pro Leu Leu Leu Leu Ser Leu Leu Val Ala Thr Trp Val
275 280 285 290

Leu Val Ala Gly Ile Tyr Leu Met Trp Arg His Glu Arg Ile Lys Lys
295 300 305

Thr Ser Phe Ser Thr Thr Thr Leu Leu Pro Pro Ile Lys Val Leu Val
310 315 320

Val Tyr Pro Ser Glu Ile Cys Phe His His Thr Ile Cys Tyr Phe Thr
325 330 335

Glu Phe Leu Gln Asn His Cys Arg Ser Glu Val Ile Leu Glu Lys Trp
340 345 350

Gln Lys Lys Lys Ile Ala Glu Met Gly Pro Val Gln Trp Leu Ala Thr
355 360 365 370

Gln Lys Lys Ala Ala Asp Lys Val Val Phe Leu Leu Ser Asn Asp Val
375 380 385

Asn Ser Val Cys Asp Gly Thr Cys Gly Lys Ser Glu Gly Ser Pro Ser
390 395 400

Glu Asn Ser Gln Asp Leu Phe Pro Leu Ala Phe Asn Leu Phe Cys Ser
405 410 415

Asp Leu Arg Ser Gln Ile His Leu His Lys Tyr Val Val Val Tyr Phe
420 425 430

Arg Glu Ile Asp Thr Lys Asp Asp Tyr Asn Ala Leu Ser Val Cys Pro
435 440 445 450

Lys Tyr His Leu Met Lys Asp Ala Thr Ala Phe Cys Ala Glu Leu Leu
455 460 465

His Val Lys Gln Gln Val Ser Ala Gly Lys Arg Ser Gln Ala Cys His
470 475 480

Asp Gly Cys Cys Ser Leu
485

<210> 3
<211> 637
<212> DNA
<213> Mus musculus

<220>
<221> CDS
<222> (1)..(210)
<223>

<400> 3
gat ttc agc agc cag acg cat ctg cac aaa tac ctg gag gtc tat ctt 48
Asp Phe Ser Ser Gln Thr His Leu His Lys Tyr Leu Glu Val Tyr Leu
1 5 10 15
ggg gga gca gac ctc aaa ggc gac tat aat gcc ctg agt gtc tgc ccc 96
Gly Gly Ala Asp Leu Lys Gly Asp Tyr Asn Ala Leu Ser Val Cys Pro
20 25 30
caa tat cat ctc atg aag gac gcc aca gct ttc cac aca gaa ctt ctc 144
Gln Tyr His Leu Met Lys Asp Ala Thr Ala Phe His Thr Glu Leu Leu
35 40 45
aag gct acg cag agc atg tca gtg aag aaa cgc tca caa gcc tgc cat 192
Lys Ala Thr Gln Ser Met Ser Val Lys Lys Arg Ser Gln Ala Cys His
50 55 60
gat agc tgt tca ccc ttg tagtccaccc gggggaatag agactctgaa 240
Asp Ser Cys Ser Pro Leu
65 70
gccttcctac tctcccttcc agtgacaaat gctgtgtgac gactctgaaa tgtgtgggag 300
aggctgtgtg gaggtagtgc tatgtacaaa cttgctttta aactggagtt tgcaaagtca 360
acctgagcat acacgcctga ggctagtcac ttgctggatt tatgaagaca acacagttac 420
agacaataat gagtgggacc tacatttggg atatacccaa agctgggtaa tgattatcac 480
tgagaaccac gcactctggc catgaggtaa tacggcactt ccctgtcagg ctgtctgtca 540
ggttgggtct gtcttgact gcccatgctc tatgctgcac gtagaccgtt ttgtaacatt 600
ttaatctgtt aatgaataat ccgtttggga ggctctc 637

<210> 4
<211> 70
<212> PRT
<213> Mus musculus

<400> 4

Asp Phe Ser Ser Gln Thr His Leu His Lys Tyr Leu Glu Val Tyr Leu
1 5 10 15

Gly Gly Ala Asp Leu Lys Gly Asp Tyr Asn Ala Leu Ser Val Cys Pro
 20 25 30

Gln Tyr His Leu Met Lys Asp Ala Thr Ala Phe His Thr Glu Leu Leu
 35 40 45

Lys Ala Thr Gln Ser Met Ser Val Lys Lys Arg Ser Gln Ala Cys His
 50 55 60

Asp Ser Cys Ser Pro Leu
 65 70

<210> 5
 <211> 2308
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (181)..(2289)
 <223>

<220>
 <221> mat_peptide
 <222> (241)..()
 <223>

<220>
 <221> misc_feature
 <222> (140)..(140)
 <223> unknown amino

<220>
 <221> misc_feature
 <222> (2232)..(2232)
 <223> unknown amino

<400> 5
 gagtcaggac tcccaggaca gagagtgcac aaactaccca gcacagcccc ctccgcccc 60
 tctggaggct gaagagggat tccagcccct gccacccaca gacacgggct gactgggggtg 120
 tctgcccccc ttgggggcan ccacagggcc tcaggcctgg gtgccacctg gcactagaag 180
 atg cct gtg ccc tgg ttc ttg ctg tcc ttg gca ctg ggc cga agc cag 228
 Met Pro Val Pro Trp Phe Leu Leu Ser Leu Ala Leu Gly Arg Ser Gln
 -20 -15 -10 -5
 tgg atc ctt tct ctg gag agg ctt gtg ggg cct cag gac gct acc cac 276
 Trp Ile Leu Ser Leu Glu Arg Leu Val Gly Pro Gln Asp Ala Thr His
 -1 1 5 10

tgc tct ccg ggc ctc tcc tgc cgc ctc tgg gac agt gac ata ctc tgc Cys Ser Pro Gly Leu Ser Cys Arg Leu Trp Asp Ser Asp Ile Leu Cys 15 20 25	324
ctg cct ggg gac atc gtg cct gct ccg ggc ccc gtg ctg gcg cct acg Leu Pro Gly Asp Ile Val Pro Ala Pro Gly Pro Val Leu Ala Pro Thr 30 35 40	372
cac ctg cag aca gag ctg gtg ctg agg tgc cag aag gag acc gac tgt His Leu Gln Thr Glu Leu Val Leu Arg Cys Gln Lys Glu Thr Asp Cys 45 50 55 60	420
gac ctc tgt ctg cgt gtg gct gtc cac ttg gcc gtg cat ggg cac tgg Asp Leu Cys Leu Arg Val Ala Val His Leu Ala Val His Gly His Trp 65 70 75	468
gaa gag cct gaa gat gag gaa aag ttt gga gga gca gct gac tta ggg Glu Glu Pro Glu Asp Glu Glu Lys Phe Gly Gly Ala Ala Asp Leu Gly 80 85 90	516
gtg gag gag cct agg aat gcc tct ctc cag gcc caa gtc gtg ctc tcc Val Glu Glu Pro Arg Asn Ala Ser Leu Gln Ala Gln Val Val Leu Ser 95 100 105	564
ttc cag gcc tac cct act gcc cgc tgc gtc ctg ctg gag gtg caa gtg Phe Gln Ala Tyr Pro Thr Ala Arg Cys Val Leu Leu Glu Val Gln Val 110 115 120	612
cct gct gcc ctt gtg cag ttt ggt cag tct gtg ggc tct gtg gta tat Pro Ala Ala Leu Val Gln Phe Gly Gln Ser Val Gly Ser Val Val Tyr 125 130 135 140	660
gac tgc ttc gag gct gcc cta ggg agt gag gta cga atc tgg tcc tat Asp Cys Phe Glu Ala Ala Leu Gly Ser Glu Val Arg Ile Trp Ser Tyr 145 150 155	708
act cag ccc agg tac gag aag gaa ctc aac cac aca cag cag ctg cct Thr Gln Pro Arg Tyr Glu Lys Glu Leu Asn His Thr Gln Gln Leu Pro 160 165 170	756
gac tgc agg ggg ctc gaa gtc tgg aac agc atc ccg agc tgc tgg gcc Asp Cys Arg Gly Leu Glu Val Trp Asn Ser Ile Pro Ser Cys Trp Ala 175 180 185	804
ctg ccc tgg ctc aac gtg tca gca gat ggt gac aac gtg cat ctg gtt Leu Pro Trp Leu Asn Val Ser Ala Asp Gly Asp Asn Val His Leu Val 190 195 200	852
ctg aat gtc tct gag gag cag cac ttc ggc ctc tcc ctg tac tgg aat Leu Asn Val Ser Glu Glu Gln His Phe Gly Leu Ser Leu Tyr Trp Asn 205 210 215 220	900
cag gtc cag ggc ccc cca aaa ccc cgg tgg cac aaa aac ctg act gga Gln Val Gln Gly Pro Pro Lys Pro Arg Trp His Lys Asn Leu Thr Gly 225 230 235	948
ccg cag atc att acc ttg aac cac aca gac ctg gtt ccc tgc ctc tgt Pro Gln Ile Ile Thr Leu Asn His Thr Asp Leu Val Pro Cys Leu Cys 240 245 250	996

att cag gtg tgg cct ctg gaa cct gac tcc gtt agg acg aac atc tgc Ile Gln Val Trp Pro Leu Glu Pro Asp Ser Val Arg Thr Asn Ile Cys 255 260 265	1044
ccc ttc agg gag gac ccc cgc gca cac cag aac ctc tgg caa gcc gcc Pro Phe Arg Glu Asp Pro Arg Ala His Gln Asn Leu Trp Gln Ala Ala 270 275 280	1092
cga ctg cga ctg ctg acc ctg cag agc tgg ctg ctg gac gca ccg tgc Arg Leu Arg Leu Leu Thr Leu Gln Ser Trp Leu Leu Asp Ala Pro Cys 285 290 295 300	1140
tcg ctg ccc gca gaa gcg gca ctg tgc tgg cgg gct ccg ggt ggg gac Ser Leu Pro Ala Glu Ala Ala Leu Cys Trp Arg Ala Pro Gly Gly Asp 305 310 315	1188
ccc tgc cag cca ctg gtc cca ccg ctt tcc tgg gag aat gtc act gtg Pro Cys Gln Pro Leu Val Pro Pro Leu Ser Trp Glu Asn Val Thr Val 320 325 330	1236
gac gtg aac agc tcg gag aag ctg cag ctg cag gag tgc ttg tgg gct Asp Val Asn Ser Ser Glu Lys Leu Gln Leu Gln Glu Cys Leu Trp Ala 335 340 345	1284
gac tcc ctg ggg cct ctc aaa gac gat gtg cta ctg ttg gag aca cga Asp Ser Leu Gly Pro Leu Lys Asp Asp Val Leu Leu Leu Glu Thr Arg 350 355 360	1332
ggc ccc cag gac aac aga tcc ctc tgt gcc ttg gaa ccc agt ggc tgt Gly Pro Gln Asp Asn Arg Ser Leu Cys Ala Leu Glu Pro Ser Gly Cys 365 370 375 380	1380
act tca cta ccc agc aaa gcc tcc acg agg gca gct cgc ctt gga gag Thr Ser Leu Pro Ser Lys Ala Ser Thr Arg Ala Ala Arg Leu Gly Glu 385 390 395	1428
tac tta cta caa gac ctg cag tca ggc cag tgt ctg cag cta tgg gac Tyr Leu Leu Gln Asp Leu Gln Ser Gly Gln Cys Leu Gln Leu Trp Asp 400 405 410	1476
gat gac ttg gga gcg cta tgg gcc tgc ccc atg gac aaa tac atc cac Asp Asp Leu Gly Ala Leu Trp Ala Cys Pro Met Asp Lys Tyr Ile His 415 420 425	1524
aag cgc tgg gcc ctc gtg tgg ctg gcc tgc cta ctc ttt gcc gct gcg Lys Arg Trp Ala Leu Val Trp Leu Ala Cys Leu Leu Phe Ala Ala 430 435 440	1572
ctt tcc ctc atc ctc ctt ctc aaa aag gat cac gcg aaa ggg tgg ctg Leu Ser Leu Ile Leu Leu Lys Lys Asp His Ala Lys Gly Trp Leu 445 450 455 460	1620
agg ctc ttg aaa cag gac gtc cgc tcg ggg gcg gcc gcc agg ggc cgc Arg Leu Leu Lys Gln Asp Val Arg Ser Gly Ala Ala Ala Arg Gly Arg 465 470 475	1668
gcg gct ctg ctc ctc tac tca gcc gat gac tcg ggt ttc gag cgc ctg Ala Ala Leu Leu Leu Tyr Ser Ala Asp Ser Gly Phe Glu Arg Leu 480 485 490	1716
gtg ggc gcc ctg gcg tcg gcc ctg tgc cag ctg ccg ctg cgc gtg gcc	1764

Val Gly Ala Leu Ala Ser Ala Leu Cys Gln Leu Pro Leu Arg Val Ala	
495 500 505	
gta gac ctg tgg agc cgt cgt gaa ctg agc gcg cag ggg ccc gtg gct	1812
Val Asp Leu Trp Ser Arg Arg Glu Leu Ser Ala Gln Gly Pro Val Ala	
510 515 520	
tgg ttt cac gcg cag cgg cgc cag acc ctg cag gag ggc ggc gtg gtg	1860
Trp Phe His Ala Gln Arg Arg Gln Thr Leu Gln Glu Gly Gly Val Val	
525 530 535 540	
gtc ttg ctc ttc tct ccc ggt gcg gtg gcg ctg tgc agc gag tgg cta	1908
Val Leu Leu Phe Ser Pro Gly Ala Val Ala Leu Cys Ser Glu Trp Leu	
545 550 555	
cag gat ggg gtg tcc ggg ccc ggg gcg cac ggc ccg cac gac gcc ttc	1956
Gln Asp Gly Val Ser Gly Pro Gly Ala His Gly Pro His Asp Ala Phe	
560 565 570	
cgc gcc tcg ctc agc tgc gtg ctg ccc gac ttc ttg cag ggc cgg gcg	2004
Arg Ala Ser Leu Ser Cys Val Leu Pro Asp Phe Leu Gln Gly Arg Ala	
575 580 585	
ccc ggc agc tac gtg ggg gcc tgc ttc gac agg ctg ctc cac ccg gac	2052
Pro Gly Ser Tyr Val Gly Ala Cys Phe Asp Arg Leu Leu His Pro Asp	
590 595 600	
gcc gta ccc gcc ctt ttc cgc acc gtg ccc gtc ttc aca ctg ccc tcc	2100
Ala Val Pro Ala Leu Phe Arg Thr Val Pro Val Phe Thr Leu Pro Ser	
605 610 615 620	
caa ctg cca gac ttc ctg ggg gcc ctg cag cag cct cgc gcc ccg cgt	2148
Gln Leu Pro Asp Phe Leu Gly Ala Leu Gln Gln Pro Arg Ala Pro Arg	
625 630 635	
tcc ggg cgg ctc caa gag aga gcg gag caa gtg tcc cgg gcc ctt cag	2196
Ser Gly Arg Leu Gln Glu Arg Ala Glu Gln Val Ser Arg Ala Leu Gln	
640 645 650	
cca gcc ctg gat agc tac ttc cat ccc ccg ggg acn tcc gcg ccg gga	2244
Pro Ala Leu Asp Ser Tyr Phe His Pro Pro Gly Xaa Ser Ala Pro Gly	
655 660 665	
cgc ggg gtg gga cca ggg gcg gga cct ggg gcg ggg gac ggg act	2289
Arg Gly Val Gly Pro Gly Ala Gly Pro Gly Ala Gly Asp Gly Thr	
670 675 680	
taaataaagg cagacgctg	2308

<210> 6
 <211> 703
 <212> PRT
 <213> Homo sapiens

 <220>
 <221> misc_feature
 <222> (664)..(664)
 <223> The 'Xaa' at location 664 stands for Thr.

 <220>

<221> misc_feature
<222> (140)..(140)
<223> unknown amino

<220>
<221> misc_feature
<222> (2232)..(2232)
<223> unknown amino

<400> 6

Met Pro Val Pro Trp Phe Leu Leu Ser Leu Ala Leu Gly Arg Ser Gln
-20 -15 -10 -5

Trp Ile Leu Ser Leu Glu Arg Leu Val Gly Pro Gln Asp Ala Thr His
-1 1 5 10

Cys Ser Pro Gly Leu Ser Cys Arg Leu Trp Asp Ser Asp Ile Leu Cys
15 20 25

Leu Pro Gly Asp Ile Val Pro Ala Pro Gly Pro Val Leu Ala Pro Thr
30 35 40

His Leu Gln Thr Glu Leu Val Leu Arg Cys Gln Lys Glu Thr Asp Cys
45 50 55 60

Asp Leu Cys Leu Arg Val Ala Val His Leu Ala Val His Gly His Trp
65 70 75

Glu Glu Pro Glu Asp Glu Glu Lys Phe Gly Gly Ala Ala Asp Leu Gly
80 85 90

Val Glu Glu Pro Arg Asn Ala Ser Leu Gln Ala Gln Val Val Leu Ser
95 100 105

Phe Gln Ala Tyr Pro Thr Ala Arg Cys Val Leu Leu Glu Val Gln Val
110 115 120

Pro Ala Ala Leu Val Gln Phe Gly Gln Ser Val Gly Ser Val Val Tyr
125 130 135 140

Asp Cys Phe Glu Ala Ala Leu Gly Ser Glu Val Arg Ile Trp Ser Tyr
145 150 155

Thr Gln Pro Arg Tyr Glu Lys Glu Leu Asn His Thr Gln Gln Leu Pro
160 165 170

Asp Cys Arg Gly Leu Glu Val Trp Asn Ser Ile Pro Ser Cys Trp Ala
175 180 185

Leu Pro Trp Leu Asn Val Ser Ala Asp Gly Asp Asn Val His Leu Val
 190 195 200

Leu Asn Val Ser Glu Glu Gln His Phe Gly Leu Ser Leu Tyr Trp Asn
 205 210 215 220

Gln Val Gln Gly Pro Pro Lys Pro Arg Trp His Lys Asn Leu Thr Gly
 225 230 235

Pro Gln Ile Ile Thr Leu Asn His Thr Asp Leu Val Pro Cys Leu Cys
 240 245 250

Ile Gln Val Trp Pro Leu Glu Pro Asp Ser Val Arg Thr Asn Ile Cys
 255 260 265

Pro Phe Arg Glu Asp Pro Arg Ala His Gln Asn Leu Trp Gln Ala Ala
 270 275 280

Arg Leu Arg Leu Leu Thr Leu Gln Ser Trp Leu Leu Asp Ala Pro Cys
 285 290 295 300

Ser Leu Pro Ala Glu Ala Ala Leu Cys Trp Arg Ala Pro Gly Gly Asp
 305 310 315

Pro Cys Gln Pro Leu Val Pro Pro Leu Ser Trp Glu Asn Val Thr Val
 320 325 330

Asp Val Asn Ser Ser Glu Lys Leu Gln Leu Gln Glu Cys Leu Trp Ala
 335 340 345

Asp Ser Leu Gly Pro Leu Lys Asp Asp Val Leu Leu Leu Glu Thr Arg
 350 355 360

Gly Pro Gln Asp Asn Arg Ser Leu Cys Ala Leu Glu Pro Ser Gly Cys
 365 370 375 380

Thr Ser Leu Pro Ser Lys Ala Ser Thr Arg Ala Ala Arg Leu Gly Glu
 385 390 395

Tyr Leu Leu Gln Asp Leu Gln Ser Gly Gln Cys Leu Gln Leu Trp Asp
 400 405 410

Asp Asp Leu Gly Ala Leu Trp Ala Cys Pro Met Asp Lys Tyr Ile His
 415 420 425

Lys Arg Trp Ala Leu Val Trp Leu Ala Cys Leu Leu Phe Ala Ala Ala
 430 435 440

Leu Ser Leu Ile Leu Leu Leu Lys Lys Asp His Ala Lys Gly Trp Leu
 445 450 455 460

Arg Leu Leu Lys Gln Asp Val Arg Ser Gly Ala Ala Ala Arg Gly Arg
 465 470 475

Ala Ala Leu Leu Leu Tyr Ser Ala Asp Asp Ser Gly Phe Glu Arg Leu
 480 485 490

Val Gly Ala Leu Ala Ser Ala Leu Cys Gln Leu Pro Leu Arg Val Ala
 495 500 505

Val Asp Leu Trp Ser Arg Arg Glu Leu Ser Ala Gln Gly Pro Val Ala
 510 515 520

Trp Phe His Ala Gln Arg Arg Gln Thr Leu Gln Glu Gly Gly Val Val
 525 530 535 540

Val Leu Leu Phe Ser Pro Gly Ala Val Ala Leu Cys Ser Glu Trp Leu
 545 550 555

Gln Asp Gly Val Ser Gly Pro Gly Ala His Gly Pro His Asp Ala Phe
 560 565 570

Arg Ala Ser Leu Ser Cys Val Leu Pro Asp Phe Leu Gln Gly Arg Ala
 575 580 585

Pro Gly Ser Tyr Val Gly Ala Cys Phe Asp Arg Leu Leu His Pro Asp
 590 595 600

Ala Val Pro Ala Leu Phe Arg Thr Val Pro Val Phe Thr Leu Pro Ser
 605 610 615 620

Gln Leu Pro Asp Phe Leu Gly Ala Leu Gln Gln Pro Arg Ala Pro Arg
 625 630 635

Ser Gly Arg Leu Gln Glu Arg Ala Glu Gln Val Ser Arg Ala Leu Gln
 640 645 650

Pro Ala Leu Asp Ser Tyr Phe His Pro Pro Gly Xaa Ser Ala Pro Gly
 655 660 665

Arg Gly Val Gly Pro Gly Ala Gly Pro Gly Ala Gly Asp Gly Thr
670 675 680

<210> 7
<211> 2314
<212> DNA
<213> Mus musculus

<220>
<221> CDS
<222> (199)..(2292)
<223>

<220>
<221> mat_peptide
<222> (259)..()
<223>

<400> 7
ccaaatcgaa agcacgggag ctgatactgg gcctggagtc caggctcact ggagtgggga 60
agcatggctg gagaggaatt ctagcccttg ctctctccca gggacacggg gctgattgtc 120
agcagggggcg aggggtctgc ccccccttgg gggggcagga cggggcctca ggctgggtg 180
ctgtccggca cctggaag atg cct gtg tcc tgg ttc ctg ctg tcc ttg gca 231
Met Pro Val Ser Trp Phe Leu Leu Ser Leu Ala
-20 -15 -10
ctg ggc cga aac cct gtg gtc gtc tct ctg gag aga ctg atg gag cct 279
Leu Gly Arg Asn Pro Val Val Val Ser Leu Glu Arg Leu Met Glu Pro
-5 -1 1 5
cag gac act gca cgc tgc tct cta ggc ctc tcc tgc cac ctc tgg gat 327
Gln Asp Thr Ala Arg Cys Ser Leu Gly Leu Ser Cys His Leu Trp Asp
10 15 20
ggt gac gtg ctc tgc ctg cct gga agc ctc cag tct gcc cca ggc cct 375
Gly Asp Val Leu Cys Leu Pro Gly Ser Leu Gln Ser Ala Pro Gly Pro
25 30 35
gtg cta gtg cct acc cgc ctg cag acg gag ctg gtg ctg agg tgt cca 423
Val Leu Val Pro Thr Arg Leu Gln Thr Glu Leu Val Leu Arg Cys Pro
40 45 50 55
cag aag aca gat tgc gcc ctc tgt gtc cgt gtg gtg gtc cac ttg gcc 471
Gln Lys Thr Asp Cys Ala Leu Cys Val Arg Val Val Val His Leu Ala
60 65 70
gtg cat ggg cac tgg gca gag cct gaa gaa gct gga aag tct gat tca 519
Val His Gly His Trp Ala Glu Pro Glu Glu Ala Gly Lys Ser Asp Ser
75 80 85
gaa ctc cag gag tct agg aac gcc tct ctc cag gcc cag gtg gtg ctc 567
Glu Leu Gln Glu Ser Arg Asn Ala Ser Leu Gln Ala Gln Val Val Leu
90 95 100
tcc ttc cag gcc tac ccc atc gcc cgc tgt gcc ctg ctg gag gtc cag 615

Ser Phe Gln Ala Tyr Pro Ile Ala Arg Cys Ala Leu Leu Glu Val Gln	
105 110 115	
gtg ccc gct gac ctg gtg cag cct ggt cag tcc gtg ggt tct gcg gta	663
Val Pro Ala Asp Leu Val Gln Pro Gly Gln Ser Val Gly Ser Ala Val	
120 125 130 135	
ttt gac tgt ttc gag gct agt ctt ggg gct gag gta cag atc tgg tcc	711
Phe Asp Cys Phe Glu Ala Ser Leu Gly Ala Glu Val Gln Ile Trp Ser	
140 145 150	
tac acg aag ccc agg tac cag aaa gag ctc aac ctc aca cag cag ctg	759
Tyr Thr Lys Pro Arg Tyr Gln Lys Glu Leu Asn Leu Thr Gln Gln Leu	
155 160 165	
cct gac tgc agg ggt ctt gaa gtc cgg gac agc atc cag agc tgc tgg	807
Pro Asp Cys Arg Gly Leu Glu Val Arg Asp Ser Ile Gln Ser Cys Trp	
170 175 180	
gtc ctg ccc tgg ctc aat gtg tct aca gat ggt gac aat gtc ctt ctg	855
Val Leu Pro Trp Leu Asn Val Ser Thr Asp Gly Asp Asn Val Leu Leu	
185 190 195	
aca ctg gat gtc tct gag gag cag gac ttt agc ttc tta ctg tac ctg	903
Thr Leu Asp Val Ser Glu Glu Gln Asp Phe Ser Phe Leu Leu Tyr Leu	
200 205 210 215	
cgt cca gtc ccg gat gct ctc aaa tcc ttg tgg tac aaa aac ctg act	951
Arg Pro Val Pro Asp Ala Leu Lys Ser Leu Trp Tyr Lys Asn Leu Thr	
220 225 230	
gga cct cag aac att act tta aac cac aca gac ctg gtt ccc tgc ctc	999
Gly Pro Gln Asn Ile Thr Leu Asn His Thr Asp Leu Val Pro Cys Leu	
235 240 245	
tgc att cag gtg tgg tcg cta gag cca gac tct gag agg gtc gaa ttc	1047
Cys Ile Gln Val Trp Ser Leu Glu Pro Asp Ser Glu Arg Val Glu Phe	
250 255 260	
tgc ccc ttc cgg gaa gat ccc ggt gca cac agg aac ctc tgg cac ata	1095
Cys Pro Phe Arg Glu Asp Pro Gly Ala His Arg Asn Leu Trp His Ile	
265 270 275	
gcc agg ctg cgg gta ctg tcc cca ggg gta tgg cag cta gat gcg cct	1143
Ala Arg Leu Arg Val Leu Ser Pro Gly Val Trp Gln Leu Asp Ala Pro	
280 285 290 295	
tgc tgt ctg ccg ggc aag gta aca ctg tgc tgg cag gca cca gac cag	1191
Cys Cys Leu Pro Gly Lys Val Thr Leu Cys Trp Gln Ala Pro Asp Gln	
300 305 310	
agt ccc tgc cag cca ctt gtg cca cca gtg ccc cag aag aac gcc act	1239
Ser Pro Cys Gln Pro Leu Val Pro Pro Val Pro Gln Lys Asn Ala Thr	
315 320 325	
gtg aat gag cca caa gat ttc cag ttg gtg gca ggc cac ccc aac ctc	1287
Val Asn Glu Pro Gln Asp Phe Gln Leu Val Ala Gly His Pro Asn Leu	
330 335 340	
tgt gtc cag gtg agc acc tgg gag aag gtt cag ctg caa gcg tgc ttg	1335
Cys Val Gln Val Ser Thr Trp Glu Lys Val Gln Leu Gln Ala Cys Leu	

345	350	355	
tgg gct gac tcc ttg ggg ccc ttc aag gat gat atg ctg tta gtg gag			1383
Trp Ala Asp Ser Leu Gly Pro Phe Lys Asp Asp Met Leu Leu Val Glu			
360	365	370	375
atg aaa acc ggc ctc aac aac aca tca gtc tgt gcc ttg gaa ccc agt			1431
Met Lys Thr Gly Leu Asn Asn Thr Ser Val Cys Ala Leu Glu Pro Ser			
	380	385	390
ggc tgt aca cca ctg ccc agc atg gcc tcc acg aga gct gct cgc ctg			1479
Gly Cys Thr Pro Leu Pro Ser Met Ala Ser Thr Arg Ala Ala Arg Leu			
	395	400	405
gga gag gag ttg ctg caa gac ttc cga tca cac cag tgt atg cag ctg			1527
Gly Glu Glu Leu Leu Gln Asp Phe Arg Ser His Gln Cys Met Gln Leu			
	410	415	420
tgg aac gat gac aac atg gga tgc cta tgg gcc tgc ccc atg gac aag			1575
Trp Asn Asp Asp Asn Met Gly Ser Leu Trp Ala Cys Pro Met Asp Lys			
	425	430	435
tac atc cac agg cgc tgg gtc cta gta tgg ctg gcc tgc cta ctc ttg			1623
Tyr Ile His Arg Arg Trp Val Leu Val Trp Leu Ala Cys Leu Leu Leu			
	440	445	450
gct gcg gcg ctt ttc ttc ttc ctc ctt cta aaa aag gac cgc agg aaa			1671
Ala Ala Ala Leu Phe Phe Leu Leu Leu Lys Lys Asp Arg Arg Lys			
	460	465	470
gcg gcc cgt ggc tcc cgc acg gcc ttg ctc ctc cac tcc gcc gac gga			1719
Ala Ala Arg Gly Ser Arg Thr Ala Leu Leu Leu His Ser Ala Asp Gly			
	475	480	485
gcg ggc tac gag cgc ctg gtg gga gca ctg gcg tcc gcg ttg agc cag			1767
Ala Gly Tyr Glu Arg Leu Val Gly Ala Leu Ala Ser Ala Leu Ser Gln			
	490	495	500
atg cca ctg cgc gtg gcc gtg gac ctg tgg agc cgc cgc gag ctg agc			1815
Met Pro Leu Arg Val Ala Val Asp Leu Trp Ser Arg Arg Glu Leu Ser			
	505	510	515
gcg cac gga gcc cta gcc tgg ttc cac cac cag cga cgc cgt atc ctg			1863
Ala His Gly Ala Leu Ala Trp Phe His His Gln Arg Arg Arg Ile Leu			
	520	525	530
cag gag ggt ggc gtg gta atc ctt ctc ttc tgc ccc gcg gcc gtg gcg			1911
Gln Glu Gly Gly Val Val Ile Leu Leu Phe Ser Pro Ala Ala Val Ala			
	540	545	550
cag tgt cag cag tgg ctg cag ctc cag aca gtg gag ccc ggg ccg cat			1959
Gln Cys Gln Gln Trp Leu Gln Leu Gln Thr Val Glu Pro Gly Pro His			
	555	560	565
gac gcc ctc gcc gcc tgg ctc agc tgc gtg cta ccc gat ttc ctg caa			2007
Asp Ala Leu Ala Ala Trp Leu Ser Cys Val Leu Pro Asp Phe Leu Gln			
	570	575	580
ggc cgg gcg acc ggc cgc tac gtc ggg gtc tac ttc gac ggg ctg ctg			2055
Gly Arg Ala Thr Gly Arg Tyr Val Gly Val Tyr Phe Asp Gly Leu Leu			
	585	590	595

cac cca gac tct gtg ccc tcc ccg ttc cgc gtc gcc ccg ctc ttc tcc 2103
 His Pro Asp Ser Val Pro Ser Pro Phe Arg Val Ala Pro Leu Phe Ser
 600 605 610 615

ctg ccc tcg cag ctg ccg gct ttc ctg gat gca ctg cag gga ggc tgc 2151
 Leu Pro Ser Gln Leu Pro Ala Phe Leu Asp Ala Leu Gln Gly Gly Cys
 620 625 630

tcc act tcc gcg ggg cga ccc gcg gac ccg gtg gaa cga gtg acc cag 2199
 Ser Thr Ser Ala Gly Arg Pro Ala Asp Arg Val Glu Arg Val Thr Gln
 635 640 645

gcg ctg ccg tcc gcc ctg gac agc tgt act tct agc tcg gaa gcc cca 2247
 Ala Leu Arg Ser Ala Leu Asp Ser Cys Thr Ser Ser Ser Glu Ala Pro
 650 655 660

ggc tgc tgc gag gaa tgg gac ctg gga ccc tgc act aca cta gaa 2292
 Gly Cys Cys Glu Glu Trp Asp Leu Gly Pro Cys Thr Thr Leu Glu
 665 670 675

taaaagccga tacagtattc ct 2314

<210> 8
 <211> 698
 <212> PRT
 <213> Mus musculus

<400> 8

Met Pro Val Ser Trp Phe Leu Leu Ser Leu Ala Leu Gly Arg Asn Pro
 -20 -15 -10 -5

Val Val Val Ser Leu Glu Arg Leu Met Glu Pro Gln Asp Thr Ala Arg
 -1 1 5 10

Cys Ser Leu Gly Leu Ser Cys His Leu Trp Asp Gly Asp Val Leu Cys
 15 20 25

Leu Pro Gly Ser Leu Gln Ser Ala Pro Gly Pro Val Leu Val Pro Thr
 30 35 40

Arg Leu Gln Thr Glu Leu Val Leu Arg Cys Pro Gln Lys Thr Asp Cys
 45 50 55 60

Ala Leu Cys Val Arg Val Val Val His Leu Ala Val His Gly His Trp
 65 70 75

Ala Glu Pro Glu Glu Ala Gly Lys Ser Asp Ser Glu Leu Gln Glu Ser
 80 85 90

Arg Asn Ala Ser Leu Gln Ala Gln Val Val Leu Ser Phe Gln Ala Tyr
 95 100 105

Pro Ile Ala Arg Cys Ala Leu Leu Glu Val Gln Val Pro Ala Asp Leu
 110 115 120

Val Gln Pro Gly Gln Ser Val Gly Ser Ala Val Phe Asp Cys Phe Glu
 125 130 135 140

Ala Ser Leu Gly Ala Glu Val Gln Ile Trp Ser Tyr Thr Lys Pro Arg
 145 150 155

Tyr Gln Lys Glu Leu Asn Leu Thr Gln Gln Leu Pro Asp Cys Arg Gly
 160 165 170

Leu Glu Val Arg Asp Ser Ile Gln Ser Cys Trp Val Leu Pro Trp Leu
 175 180 185

Asn Val Ser Thr Asp Gly Asp Asn Val Leu Leu Thr Leu Asp Val Ser
 190 195 200

Glu Glu Gln Asp Phe Ser Phe Leu Leu Tyr Leu Arg Pro Val Pro Asp
 205 210 215 220

Ala Leu Lys Ser Leu Trp Tyr Lys Asn Leu Thr Gly Pro Gln Asn Ile
 225 230 235

Thr Leu Asn His Thr Asp Leu Val Pro Cys Leu Cys Ile Gln Val Trp
 240 245 250

Ser Leu Glu Pro Asp Ser Glu Arg Val Glu Phe Cys Pro Phe Arg Glu
 255 260 265

Asp Pro Gly Ala His Arg Asn Leu Trp His Ile Ala Arg Leu Arg Val
 270 275 280

Leu Ser Pro Gly Val Trp Gln Leu Asp Ala Pro Cys Cys Leu Pro Gly
 285 290 295 300

Lys Val Thr Leu Cys Trp Gln Ala Pro Asp Gln Ser Pro Cys Gln Pro
 305 310 315

Leu Val Pro Pro Val Pro Gln Lys Asn Ala Thr Val Asn Glu Pro Gln
 320 325 330

Asp Phe Gln Leu Val Ala Gly His Pro Asn Leu Cys Val Gln Val Ser
 335 340 345

Thr Trp Glu Lys Val Gln Leu Gln Ala Cys Leu Trp Ala Asp Ser Leu
 350 355 360

Gly Pro Phe Lys Asp Asp Met Leu Leu Val Glu Met Lys Thr Gly Leu
 365 370 375 380

Asn Asn Thr Ser Val Cys Ala Leu Glu Pro Ser Gly Cys Thr Pro Leu
 385 390 395

Pro Ser Met Ala Ser Thr Arg Ala Ala Arg Leu Gly Glu Glu Leu Leu
 400 405 410

Gln Asp Phe Arg Ser His Gln Cys Met Gln Leu Trp Asn Asp Asp Asn
 415 420 425

Met Gly Ser Leu Trp Ala Cys Pro Met Asp Lys Tyr Ile His Arg Arg
 430 435 440

Trp Val Leu Val Trp Leu Ala Cys Leu Leu Leu Ala Ala Ala Leu Phe
 445 450 455 460

Phe Phe Leu Leu Leu Lys Lys Asp Arg Arg Lys Ala Ala Arg Gly Ser
 465 470 475

Arg Thr Ala Leu Leu Leu His Ser Ala Asp Gly Ala Gly Tyr Glu Arg
 480 485 490

Leu Val Gly Ala Leu Ala Ser Ala Leu Ser Gln Met Pro Leu Arg Val
 495 500 505

Ala Val Asp Leu Trp Ser Arg Arg Glu Leu Ser Ala His Gly Ala Leu
 510 515 520

Ala Trp Phe His His Gln Arg Arg Arg Ile Leu Gln Glu Gly Gly Val
 525 530 535 540

Val Ile Leu Leu Phe Ser Pro Ala Ala Val Ala Gln Cys Gln Gln Trp
 545 550 555

Leu Gln Leu Gln Thr Val Glu Pro Gly Pro His Asp Ala Leu Ala Ala
 560 565 570

Trp Leu Ser Cys Val Leu Pro Asp Phe Leu Gln Gly Arg Ala Thr Gly
 575 580 585

Arg Tyr Val Gly Val Tyr Phe Asp Gly Leu Leu His Pro Asp Ser Val
590 595 600

Pro Ser Pro Phe Arg Val Ala Pro Leu Phe Ser Leu Pro Ser Gln Leu
605 610 615 620

Pro Ala Phe Leu Asp Ala Leu Gln Gly Gly Cys Ser Thr Ser Ala Gly
625 630 635

Arg Pro Ala Asp Arg Val Glu Arg Val Thr Gln Ala Leu Arg Ser Ala
640 645 650

Leu Asp Ser Cys Thr Ser Ser Ser Glu Ala Pro Gly Cys Cys Glu Glu
655 660 665

Trp Asp Leu Gly Pro Cys Thr Thr Leu Glu
670 675

<210> 9
<211> 2786
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (70)..(2283)
<223>

<220>
<221> mat_peptide
<222> (118)..()
<223>

<220>
<221> misc_feature
<222> (8)..(8)
<223> unknown amino

<220>
<221> misc_feature
<222> (144)..(144)
<223> unknown amino

<220>
<221> misc_feature
<222> (170)..(170)
<223> unknown amino

<220>
<221> misc_feature

<222> (194)..(194)
<223> unknown amino

<220>
<221> misc_feature
<222> (442)..(442)
<223> unknown amino

<220>
<221> misc_feature
<222> (475)..(475)
<223> unknown amino

<220>
<221> misc_feature
<222> (519)..(519)
<223> unknown amino

<400> 9
cccacgcntc cgggccagca gcgggcggcc ggggcgcaga gaacggcctg gctgggcgag 60
cgacaggcc atg gcc ccg tgg ctg cag ctc tgc tcc gtc ttc ttt acg gtc 111
Met Ala Pro Trp Leu Gln Leu Cys Ser Val Phe Phe Thr Val
-15 -10 -5
aac gcc tgc ctc aac ggc tcg cag ctg gct gtn gcc gct ggc ggg tcc 159
Asn Ala Cys Leu Asn Gly Ser Gln Leu Ala Val Ala Ala Gly Gly Ser
-1 1 5 10
ggc cgc gcg cng ggc gcc gac acc tgt agc tgg ang gga gtg ggg cca 207
Gly Arg Ala Xaa Gly Ala Asp Thr Cys Ser Trp Xaa Gly Val Gly Pro
15 20 25 30
gcc agc aga aac agt ggg ctg tac aac atc acc ttc aaa tat gac aat 255
Ala Ser Arg Asn Ser Gly Leu Tyr Asn Ile Thr Phe Lys Tyr Asp Asn
35 40 45
tgt acc acc tac ttg aat cca gtg ggg aag cat gtg att gct gac gcc 303
Cys Thr Thr Tyr Leu Asn Pro Val Gly Lys His Val Ile Ala Asp Ala
50 55 60
cag aat atc acc atc agc cag tat gct tgc cat gac caa gtg gca gtc 351
Gln Asn Ile Thr Ile Ser Gln Tyr Ala Cys His Asp Gln Val Ala Val
65 70 75
acc att ctt tgg tcc cca ggg gcc ctc ggc atc gaa ttc ctg aaa gga 399
Thr Ile Leu Trp Ser Pro Gly Ala Leu Gly Ile Glu Phe Leu Lys Gly
80 85 90
ttt cgg gta ata ctg gag gag ctg aag tgc gag gga aga cag ngc caa 447
Phe Arg Val Ile Leu Glu Glu Leu Lys Ser Glu Gly Arg Gln Xaa Gln
95 100 105 110
caa ctg att cta aag gat ccg aag cag ntc aac agt agc ttc aaa aga 495
Gln Leu Ile Leu Lys Asp Pro Lys Gln Xaa Asn Ser Ser Phe Lys Arg
115 120 125

act gga atg gaa tct caa cct ttn ctg aat atg aaa ttt gaa acg gat	543
Thr Gly Met Glu Ser Gln Pro Xaa Leu Asn Met Lys Phe Glu Thr Asp	
130 135 140	
tat ttc gta agg ttg tcc ttt tcc ttc att aaa aac gaa agc aat tac	591
Tyr Phe Val Arg Leu Ser Phe Ser Phe Ile Lys Asn Glu Ser Asn Tyr	
145 150 155	
cac cct ttc ttc ttt aga acc cga gcc tgt gac ctg ttg tta cag ccg	639
His Pro Phe Phe Phe Arg Thr Arg Ala Cys Asp Leu Leu Leu Gln Pro	
160 165 170	
gac aat cta gct tgt aaa ccc ttc tgg aag cct cgg aac ctg aac atc	687
Asp Asn Leu Ala Cys Lys Pro Phe Trp Lys Pro Arg Asn Leu Asn Ile	
175 180 185 190	
agc cag cat ggc tcg gac atg cag gtg tcc ttc gac cac gca ccg cac	735
Ser Gln His Gly Ser Asp Met Gln Val Ser Phe Asp His Ala Pro His	
195 200 205	
aac ttc ggc ttc cgt ttc ttc tat ctt cac tac aag ctc aag cac gaa	783
Asn Phe Gly Phe Arg Phe Phe Tyr Leu His Tyr Lys Leu Lys His Glu	
210 215 220	
gga cct ttc aag cga aag acc tgt aag cag gag caa act aca gag atg	831
Gly Pro Phe Lys Arg Lys Thr Cys Lys Gln Glu Gln Thr Thr Glu Met	
225 230 235	
acc agc tgc ctc ctt caa aat gtt tct cca ggg gat tat ata att gag	879
Thr Ser Cys Leu Leu Gln Asn Val Ser Pro Gly Asp Tyr Ile Ile Glu	
240 245 250	
ctg gtg gat gac act aac aca aca aga aaa gtg atg cat tat gcc tta	927
Leu Val Asp Asp Thr Asn Thr Thr Arg Lys Val Met His Tyr Ala Leu	
255 260 265 270	
aag cca gtg cac tcc ccg tgg gcc ggg ccc atc aga gcc gtg gcc atc	975
Lys Pro Val His Ser Pro Trp Ala Gly Pro Ile Arg Ala Val Ala Ile	
275 280 285	
aca gtg cca ctg gta gtc ata tcg gca ttc gcg acg ctc ttc act gtg	1023
Thr Val Pro Leu Val Val Ile Ser Ala Phe Ala Thr Leu Phe Thr Val	
290 295 300	
atg tgc cgc aag aag caa caa gaa aat ata tat tca cat tta gat gaa	1071
Met Cys Arg Lys Lys Gln Gln Glu Asn Ile Tyr Ser His Leu Asp Glu	
305 310 315	
gag agc tct gag tct tcc aca tac act gca gca ctc cca aga gag agg	1119
Glu Ser Ser Glu Ser Ser Thr Tyr Thr Ala Ala Leu Pro Arg Glu Arg	
320 325 330	
ctc cgg ccg ccg ccg aag gtc ttt ctc tgc tat tcc agt aaa gat ggc	1167
Leu Arg Pro Arg Pro Lys Val Phe Leu Cys Tyr Ser Ser Lys Asp Gly	
335 340 345 350	
cag aat cac atg aat gtc gtc cag tgt ttc gcc tac ttc ctc cag gac	1215
Gln Asn His Met Asn Val Val Gln Cys Phe Ala Tyr Phe Leu Gln Asp	
355 360 365	
ttc tgt ggc tgt gag gtg gct ctg gac ctg tgg gaa gac ttc agc ctc	1263

Phe Cys Gly Cys Glu Val Ala Leu Asp Leu Trp Glu Asp Phe Ser Leu	
370 375 380	
tgt aga gaa ggg cag aga gaa tgg gtc atc cag aag atc cac gag tcc	1311
Cys Arg Glu Gly Gln Arg Glu Trp Val Ile Gln Lys Ile His Glu Ser	
385 390 395	
cag ttc atc att gtg gtt tgt tcc aaa ggt atg aag tac ttt gtg gac	1359
Gln Phe Ile Ile Val Val Cys Ser Lys Gly Met Lys Tyr Phe Val Asp	
400 405 410	
aag aag aac tac aaa cac aaa gga ggt ggc cga ggc tcg ggg aaa gga	1407
Lys Lys Asn Tyr Lys His Lys Gly Gly Gly Arg Gly Ser Gly Lys Gly	
415 420 425 430	
gag ctc ttc ctg gtg gcg gtg tca gcc att gcc gaa aag ctc cgc cag	1455
Glu Leu Phe Leu Val Ala Val Ser Ala Ile Ala Glu Lys Leu Arg Gln	
435 440 445	
gcc aag cag agt tcg tcc gcg gcg ctc agc aag ttt atc gcc gtc tac	1503
Ala Lys Gln Ser Ser Ala Ala Leu Ser Lys Phe Ile Ala Val Tyr	
450 455 460	
ttt gat tat tcc tgc gag gga gac gtc ccc ggt atc cta gac ctg agt	1551
Phe Asp Tyr Ser Cys Glu Gly Asp Val Pro Gly Ile Leu Asp Leu Ser	
465 470 475	
acc aag tac aga ctc atg gac aat ctt cct cag ctc tgt tcc cac ctg	1599
Thr Lys Tyr Arg Leu Met Asp Asn Leu Pro Gln Leu Cys Ser His Leu	
480 485 490	
cac tcc cga gac cac ggc ctc cag gag ccg ggg cag cac acg cga cag	1647
His Ser Arg Asp His Gly Leu Gln Glu Pro Gly Gln His Thr Arg Gln	
495 500 505 510	
ggc agc aga agg aac tac ttc cgg agc aag tca ggc cgg tcc cta tac	1695
Gly Ser Arg Arg Asn Tyr Phe Arg Ser Lys Ser Gly Arg Ser Leu Tyr	
515 520 525	
gtc gcc att tgc aac atg cac cag ttt att gac gag gag ccc gac tgg	1743
Val Ala Ile Cys Asn Met His Gln Phe Ile Asp Glu Glu Pro Asp Trp	
530 535 540	
ttc gaa aag cag ttc gtt ccc ttc cat cct cct cca ctg cgc tac cgg	1791
Phe Glu Lys Gln Phe Val Pro Phe His Pro Pro Pro Leu Arg Tyr Arg	
545 550 555	
gag cca gtc ttg gag aaa ttt gat tcg ggc ttg gtt tta aat gat gtc	1839
Glu Pro Val Leu Glu Lys Phe Asp Ser Gly Leu Val Leu Asn Asp Val	
560 565 570	
atg tgc aaa cca ggg cct gag agt gac ttc tgc cta aag gta gag gcg	1887
Met Cys Lys Pro Gly Pro Glu Ser Asp Phe Cys Leu Lys Val Glu Ala	
575 580 585 590	
gct gtt ctt ggg gca acc gga cca gcc gac tcc cag cac gag agt cag	1935
Ala Val Leu Gly Ala Thr Gly Pro Ala Asp Ser Gln His Glu Ser Gln	
595 600 605	
cat ggg ggc ctg gac caa gac ggg gag gcc cgg cct gcc ctt gac ggt	1983
His Gly Gly Leu Asp Gln Asp Gly Glu Ala Arg Pro Ala Leu Asp Gly	

610	615	620	
agc gcc gcc ctg caa ccc ctg ctg	cac acg gtg aaa gcc ggc agc ccc		2031
Ser Ala Ala Leu Gln Pro Leu Leu	His Thr Val Lys Ala Gly Ser Pro		
625	630	635	
tcg gac atg ccg cgg gac tca ggc atc tat	gac tcg tct gtg ccc tca		2079
Ser Asp Met Pro Arg Asp Ser Gly Ile Tyr	Asp Ser Ser Val Pro Ser		
640	645	650	
tcc gag ctg tct ctg cca ctg atg gaa gga ctc	tcg acg gac cag aca		2127
Ser Glu Leu Ser Leu Pro Leu Met Glu Gly Leu	Ser Thr Asp Gln Thr		
655	660	665	670
gaa acg tct tcc ctg acg gag agc gtg tcc tcc tct	tca ggc ctg ggt		2175
Glu Thr Ser Ser Leu Thr Glu Ser Val Ser Ser Ser	Ser Ser Gly Leu Gly		
675	680	685	
gag gag gaa cct cct gcc ctt cct tcc aag ctc ctc	tct tct ggg tca		2223
Glu Glu Glu Pro Pro Ala Leu Pro Ser Lys Leu Leu	Ser Ser Gly Ser		
690	695	700	
tgc aaa gca gat ctt ggt tgc cgc agc tac act gat	gaa ctc cac gcg		2271
Cys Lys Ala Asp Leu Gly Cys Arg Ser Tyr Thr Asp	Glu Leu His Ala		
705	710	715	
gtc gcc cct ttg taacaaaacg aaagagtcta agcattgcc	ctttagctgc		2323
Val Ala Pro Leu			
720			
tgccctccctc tgattcccca gctcatctcc ctgggttgc	at ggcccacttg gagctgaggt		2383
ctcatacaag gatatttgga gtgaaatgct ggccagtact	tggttctccct tgccccaacc		2443
ctttaccgga tatcttgaca aactctccaa ttttctaaaa	tgatatggag ctctgaaagg		2503
catgtccata aggtctgaca acagcttgcc aaatttggtt	agtccttgga tcagagcctg		2563
ttgtgggagg tagggaggaa atatgtaaag aaaaacagga	agatacctgc actaatcatt		2623
cagacttcat tgagctctgc aaactttgcc tgtttgctat	tggctacctt gatttgaaat		2683
gctttgtgaa aaaaggcact tttaacatca tagccacaga	aatcaagtgc cagtctatct		2743
ggaatccatg ttgtattgca gataatgttc tcatttattt	ttg		2786

<210> 10
 <211> 738
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (18)..(18)
 <223> The 'Xaa' at location 18 stands for Gln, Arg, Pro, or Leu.

 <220>
 <221> misc_feature
 <222> (26)..(26)
 <223> The 'Xaa' at location 26 stands for Lys, Arg, Thr, or Met.


```

<220>
<221> misc_feature
<222> (109)..(109)
<223> The 'Xaa' at location 109 stands for Ser, Gly, Arg, or Cys.

<220>
<221> misc_feature
<222> (120)..(120)
<223> The 'Xaa' at location 120 stands for Ile, Val, Leu, or Phe.

<220>
<221> misc_feature
<222> (134)..(134)
<223> The 'Xaa' at location 134 stands for Leu, or Phe.

<220>
<221> misc_feature
<222> (8)..(8)
<223> unknown amino

<220>
<221> misc_feature
<222> (144)..(144)
<223> unknown amino

<220>
<221> misc_feature
<222> (170)..(170)
<223> unknown amino

<220>
<221> misc_feature
<222> (194)..(194)
<223> unknown amino

<220>
<221> misc_feature
<222> (442)..(442)
<223> unknown amino

<220>
<221> misc_feature
<222> (475)..(475)
<223> unknown amino

<220>
<221> misc_feature
<222> (519)..(519)
<223> unknown amino

<400> 10

```

```

Met Ala Pro Trp Leu Gln Leu Cys Ser Val Phe Phe Thr Val Asn Ala
  -15                -10                -5                -1

```

```

Cys Leu Asn Gly Ser Gln Leu Ala Val Ala Ala Gly Gly Ser Gly Arg
  1              5              10              15

```

Ala Xaa Gly Ala Asp Thr Cys Ser Trp Xaa Gly Val Gly Pro Ala Ser
 20 25 30

Arg Asn Ser Gly Leu Tyr Asn Ile Thr Phe Lys Tyr Asp Asn Cys Thr
 35 40 45

Thr Tyr Leu Asn Pro Val Gly Lys His Val Ile Ala Asp Ala Gln Asn
 50 55 60

Ile Thr Ile Ser Gln Tyr Ala Cys His Asp Gln Val Ala Val Thr Ile
 65 70 75 80

Leu Trp Ser Pro Gly Ala Leu Gly Ile Glu Phe Leu Lys Gly Phe Arg
 85 90 95

Val Ile Leu Glu Glu Leu Lys Ser Glu Gly Arg Gln Xaa Gln Gln Leu
 100 105 110

Ile Leu Lys Asp Pro Lys Gln Xaa Asn Ser Ser Phe Lys Arg Thr Gly
 115 120 125

Met Glu Ser Gln Pro Xaa Leu Asn Met Lys Phe Glu Thr Asp Tyr Phe
 130 135 140

Val Arg Leu Ser Phe Ser Phe Ile Lys Asn Glu Ser Asn Tyr His Pro
 145 150 155 160

Phe Phe Phe Arg Thr Arg Ala Cys Asp Leu Leu Leu Gln Pro Asp Asn
 165 170 175

Leu Ala Cys Lys Pro Phe Trp Lys Pro Arg Asn Leu Asn Ile Ser Gln
 180 185 190

His Gly Ser Asp Met Gln Val Ser Phe Asp His Ala Pro His Asn Phe
 195 200 205

Gly Phe Arg Phe Phe Tyr Leu His Tyr Lys Leu Lys His Glu Gly Pro
 210 215 220

Phe Lys Arg Lys Thr Cys Lys Gln Glu Gln Thr Thr Glu Met Thr Ser
 225 230 235 240

Cys Leu Leu Gln Asn Val Ser Pro Gly Asp Tyr Ile Ile Glu Leu Val
 245 250 255

Asp Asp Thr Asn Thr Thr Arg Lys Val Met His Tyr Ala Leu Lys Pro

260

265

270

Val His Ser Pro Trp Ala Gly Pro Ile Arg Ala Val Ala Ile Thr Val
 275 280 285

Pro Leu Val Val Ile Ser Ala Phe Ala Thr Leu Phe Thr Val Met Cys
 290 295 300

Arg Lys Lys Gln Gln Glu Asn Ile Tyr Ser His Leu Asp Glu Glu Ser
 305 310 315 320

Ser Glu Ser Ser Thr Tyr Thr Ala Ala Leu Pro Arg Glu Arg Leu Arg
 325 330 335

Pro Arg Pro Lys Val Phe Leu Cys Tyr Ser Ser Lys Asp Gly Gln Asn
 340 345 350

His Met Asn Val Val Gln Cys Phe Ala Tyr Phe Leu Gln Asp Phe Cys
 355 360 365

Gly Cys Glu Val Ala Leu Asp Leu Trp Glu Asp Phe Ser Leu Cys Arg
 370 375 380

Glu Gly Gln Arg Glu Trp Val Ile Gln Lys Ile His Glu Ser Gln Phe
 385 390 395 400

Ile Ile Val Val Cys Ser Lys Gly Met Lys Tyr Phe Val Asp Lys Lys
 405 410 415

Asn Tyr Lys His Lys Gly Gly Gly Arg Gly Ser Gly Lys Gly Glu Leu
 420 425 430

Phe Leu Val Ala Val Ser Ala Ile Ala Glu Lys Leu Arg Gln Ala Lys
 435 440 445

Gln Ser Ser Ser Ala Ala Leu Ser Lys Phe Ile Ala Val Tyr Phe Asp
 450 455 460

Tyr Ser Cys Glu Gly Asp Val Pro Gly Ile Leu Asp Leu Ser Thr Lys
 465 470 475 480

Tyr Arg Leu Met Asp Asn Leu Pro Gln Leu Cys Ser His Leu His Ser
 485 490 495

Arg Asp His Gly Leu Gln Glu Pro Gly Gln His Thr Arg Gln Gly Ser
 500 505 510

Arg Arg Asn Tyr Phe Arg Ser Lys Ser Gly Arg Ser Leu Tyr Val Ala
515 520 525

Ile Cys Asn Met His Gln Phe Ile Asp Glu Glu Pro Asp Trp Phe Glu
530 535 540

Lys Gln Phe Val Pro Phe His Pro Pro Pro Leu Arg Tyr Arg Glu Pro
545 550 555 560

Val Leu Glu Lys Phe Asp Ser Gly Leu Val Leu Asn Asp Val Met Cys
565 570 575

Lys Pro Gly Pro Glu Ser Asp Phe Cys Leu Lys Val Glu Ala Ala Val
580 585 590

Leu Gly Ala Thr Gly Pro Ala Asp Ser Gln His Glu Ser Gln His Gly
595 600 605

Gly Leu Asp Gln Asp Gly Glu Ala Arg Pro Ala Leu Asp Gly Ser Ala
610 615 620

Ala Leu Gln Pro Leu Leu His Thr Val Lys Ala Gly Ser Pro Ser Asp
625 630 635 640

Met Pro Arg Asp Ser Gly Ile Tyr Asp Ser Ser Val Pro Ser Ser Glu
645 650 655

Leu Ser Leu Pro Leu Met Glu Gly Leu Ser Thr Asp Gln Thr Glu Thr
660 665 670

Ser Ser Leu Thr Glu Ser Val Ser Ser Ser Ser Gly Leu Gly Glu Glu
675 680 685

Glu Pro Pro Ala Leu Pro Ser Lys Leu Leu Ser Ser Gly Ser Cys Lys
690 695 700

Ala Asp Leu Gly Cys Arg Ser Tyr Thr Asp Glu Leu His Ala Val Ala
705 710 715 720

Pro Leu

<210> 11
<211> 2012
<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(1971)

<223>

<220>

<221> mat_peptide

<222> (70)..()

<223>

<400> 11

atg ggg agc tcc aga ctg gca gcc ctg ctc ctg cct ctc ctc ctc ata	48
Met Gly Ser Ser Arg Leu Ala Ala Leu Leu Leu Pro Leu Leu Leu Ile	
-20 -15 -10	
gtc atc gac ctc tct gac tct gct ggg att ggc ttt cgc cac ctg ccc	96
Val Ile Asp Leu Ser Asp Ser Ala Gly Ile Gly Phe Arg His Leu Pro	
-5 -1 1 5	
cac tgg aac acc cgc tgt cct ctg gcc tcc cac acg gaa gtt ctg cct	144
His Trp Asn Thr Arg Cys Pro Leu Ala Ser His Thr Glu Val Leu Pro	
10 15 20 25	
ata tcc ctt gcc gca cct ggt ggg ccc tct tct cca caa agc ctt ggt	192
Ile Ser Leu Ala Ala Pro Gly Gly Pro Ser Ser Pro Gln Ser Leu Gly	
30 35 40	
gtg tgc gag tct ggc act gtt ccc gct gtt tgt gcc agc atc tgc tgt	240
Val Cys Glu Ser Gly Thr Val Pro Ala Val Cys Ala Ser Ile Cys Cys	
45 50 55	
cag gtg gct cag gtc ttc aac ggg gcc tct tcc acc tcc tgg tgc aga	288
Gln Val Ala Gln Val Phe Asn Gly Ala Ser Ser Thr Ser Trp Cys Arg	
60 65 70	
aat cca aaa agt ctt cca cat tca agt tct ata gga gac aca aga tgc	336
Asn Pro Lys Ser Leu Pro His Ser Ser Ser Ile Gly Asp Thr Arg Cys	
75 80 85	
cag cac ctg ctc aga gga agc tgc tgc ctc gtc gtc acc tgt ctg aga	384
Gln His Leu Leu Arg Gly Ser Cys Cys Leu Val Val Thr Cys Leu Arg	
90 95 100 105	
aga gcc atc aca ttt cca tcc cct ccc cag aca tct ccc aca agg gac	432
Arg Ala Ile Thr Phe Pro Ser Pro Pro Gln Thr Ser Pro Thr Arg Asp	
110 115 120	
ttc gct cta aaa gga ccc aac ctt cgg atc cag aga cat ggg aaa gtc	480
Phe Ala Leu Lys Gly Pro Asn Leu Arg Ile Gln Arg His Gly Lys Val	
125 130 135	
ttc cca gat tgg act cac aaa ggc atg gag gtg ggc act ggg tac aac	528
Phe Pro Asp Trp Thr His Lys Gly Met Glu Val Gly Thr Gly Tyr Asn	
140 145 150	
agg aga tgg gtt cag ctg agt ggt gga ccc gag ttc tcc ttt gat ttg	576
Arg Arg Trp Val Gln Leu Ser Gly Gly Pro Glu Phe Ser Phe Asp Leu	

155	160	165	
ctg cct gag gcc cgg gct att cgg gtg acc ata tct tca ggc cct gag Leu Pro Glu Ala Arg Ala Ile Arg Val Thr Ile Ser Ser Gly Pro Glu 170 175 180 185			624
gtc agc gtg cgt ctt tgt cac cag tgg gca ctg gag tgt gaa gag ctg Val Ser Val Arg Leu Cys His Gln Trp Ala Leu Glu Cys Glu Glu Leu 190 195 200			672
agc agt ccc tat gat gtc cag aaa att gtg tct ggg ggc cac act gta Ser Ser Pro Tyr Asp Val Gln Lys Ile Val Ser Gly Gly His Thr Val 205 210 215			720
gag ctg cct tat gaa ttc ctt ctg ccc tgt ctg tgc ata gag gca tcc Glu Leu Pro Tyr Glu Phe Leu Leu Pro Cys Leu Cys Ile Glu Ala Ser 220 225 230			768
tac ctg caa gag gac act gtg agg cgc aaa aaa tgt ccc ttc cag agc Tyr Leu Gln Glu Asp Thr Val Arg Arg Lys Lys Cys Pro Phe Gln Ser 235 240 245			816
tgg cca gaa gcc tat ggc tgc gac ttc tgg aag tca gtg cac ttc act Trp Pro Glu Ala Tyr Gly Ser Asp Phe Trp Lys Ser Val His Phe Thr 250 255 260 265			864
gac tac agc cag cac act cag atg gtc atg gcc ctg aca ctc cgc tgc Asp Tyr Ser Gln His Thr Gln Met Val Met Ala Leu Thr Leu Arg Cys 270 275 280			912
cca ctg aag ctg gaa gct gcc ctc tgc cag agg cac gac tgg cat acc Pro Leu Lys Leu Glu Ala Ala Leu Cys Gln Arg His Asp Trp His Thr 285 290 295			960
ctt tgc aaa gac ctc ccg aat gcc acg gct cga gag tca gat ggg tgg Leu Cys Lys Asp Leu Pro Asn Ala Thr Ala Arg Glu Ser Asp Gly Trp 300 305 310			1008
tat gtt ttg gag aag gtg gac ctg cac ccc cag ctc tgc ttc aag gta Tyr Val Leu Glu Lys Val Asp Leu His Pro Gln Leu Cys Phe Lys Val 315 320 325			1056
caa cca tgg ttc tct ttt gga aac agc agc cat gtt gaa tgc ccc cac Gln Pro Trp Phe Ser Phe Gly Asn Ser Ser His Val Glu Cys Pro His 330 335 340 345			1104
cag act ggg tct ctc aca tcc tgg aat gta agc atg gat acc caa gcc Gln Thr Gly Ser Leu Thr Ser Trp Asn Val Ser Met Asp Thr Gln Ala 350 355 360			1152
cag cag ctg att ctt cac ttc tcc tca aga atg cat gcc acc ttc agt Gln Gln Leu Ile Leu His Phe Ser Ser Arg Met His Ala Thr Phe Ser 365 370 375			1200
gct gcc tgg agc ctc cca ggc ttg ggg cag gac act ttg gtg ccc ccc Ala Ala Trp Ser Leu Pro Gly Leu Gly Gln Asp Thr Leu Val Pro Pro 380 385 390			1248
gtg tac act gtc agc cag gtg tgg cgg tca gat gtc cag ttt gcc tgg Val Tyr Thr Val Ser Gln Val Trp Arg Ser Asp Val Gln Phe Ala Trp 395 400 405			1296

aag cac ctc ttg tgt cca gat gtc tct tac aga cac ctg ggg ctc ttg Lys His Leu Leu Cys Pro Asp Val Ser Tyr Arg His Leu Gly Leu Leu 410 415 420 425	1344
atc ctg gca ctg ctg gcc ctc ctc acc cta ctg ggt gtt gtt ctg gcc Ile Leu Ala Leu Leu Ala Leu Leu Thr Leu Leu Gly Val Val Leu Ala 430 435 440	1392
ctc acc tgc cgg cgc cca cag tca ggc ccg ggc cca gcg cgg cca gtg Leu Thr Cys Arg Arg Pro Gln Ser Gly Pro Gly Pro Ala Arg Pro Val 445 450 455	1440
ctc ctc ctg cac gcg gcg gac tcg gag gcg cag cgg cgc ctg gtg gga Leu Leu Leu His Ala Ala Asp Ser Glu Ala Gln Arg Arg Leu Val Gly 460 465 470	1488
gcg ctg gct gaa ctg cta cgg gca gcg ctg ggc ggc ggg cgc gac gtg Ala Leu Ala Glu Leu Leu Arg Ala Ala Leu Gly Gly Gly Arg Asp Val 475 480 485	1536
atc gtg gac ctg tgg gag ggg agg cac gtg gcg cgc gtg ggc ccg ctg Ile Val Asp Leu Trp Glu Gly Arg His Val Ala Arg Val Gly Pro Leu 490 495 500 505	1584
ccg tgg ctc tgg gcg gcg cgg acg cgc gta gcg cgg gag cag ggc act Pro Trp Leu Trp Ala Ala Arg Thr Arg Val Ala Arg Glu Gln Gly Thr 510 515 520	1632
gtg ctg ctg ctg tgg agc ggc gcc gac ctt cgc ccg gtc agc ggc ccc Val Leu Leu Leu Trp Ser Gly Ala Asp Leu Arg Pro Val Ser Gly Pro 525 530 535	1680
gac ccc cgc gcc gcg ccc ctg ctc gcc ctg ctc cac gct gcc ccg cgc Asp Pro Arg Ala Ala Pro Leu Leu Ala Leu Leu His Ala Ala Pro Arg 540 545 550	1728
ccg ctg ctg ctg ctc gct tac ttc agt cgc ctc tgc gcc aag ggc gac Pro Leu Leu Leu Leu Ala Tyr Phe Ser Arg Leu Cys Ala Lys Gly Asp 555 560 565	1776
atc ccc ccg ccg ctg cgc gcc ctg ccg cgc tac cgc ctg ctg cgc gac Ile Pro Pro Pro Leu Arg Ala Leu Pro Arg Tyr Arg Leu Leu Arg Asp 570 575 580 585	1824
ctg ccg cgt ctg ctg cgg gcg ctg gac gcg cgg cct ttc gca gag gcc Leu Pro Arg Leu Leu Arg Ala Leu Asp Ala Arg Pro Phe Ala Glu Ala 590 595 600	1872
acc agc tgg ggc cgc ctt ggg gcg cgg cag cgc agg cag agc cgc cta Thr Ser Trp Gly Arg Leu Gly Ala Arg Gln Arg Arg Gln Ser Arg Leu 605 610 615	1920
gag ctg tgc agc cgg ctc gaa cga gag gcc gcc cga ctt gca gac cta Glu Leu Cys Ser Arg Leu Glu Arg Glu Ala Ala Arg Leu Ala Asp Leu 620 625 630	1968
ggg tgagcagagc tccaccgcag tcccgggtgt ctgcggccgc t Gly	2012

<210> 12
<211> 657
<212> PRT
<213> Homo sapiens

<400> 12

Met Gly Ser Ser Arg Leu Ala Ala Leu Leu Leu Pro Leu Leu Leu Ile
-20 -15 -10

Val Ile Asp Leu Ser Asp Ser Ala Gly Ile Gly Phe Arg His Leu Pro
-5 -1 1 5

His Trp Asn Thr Arg Cys Pro Leu Ala Ser His Thr Glu Val Leu Pro
10 15 20 25

Ile Ser Leu Ala Ala Pro Gly Gly Pro Ser Ser Pro Gln Ser Leu Gly
30 35 40

Val Cys Glu Ser Gly Thr Val Pro Ala Val Cys Ala Ser Ile Cys Cys
45 50 55

Gln Val Ala Gln Val Phe Asn Gly Ala Ser Ser Thr Ser Trp Cys Arg
60 65 70

Asn Pro Lys Ser Leu Pro His Ser Ser Ser Ile Gly Asp Thr Arg Cys
75 80 85

Gln His Leu Leu Arg Gly Ser Cys Cys Leu Val Val Thr Cys Leu Arg
90 95 100 105

Arg Ala Ile Thr Phe Pro Ser Pro Pro Gln Thr Ser Pro Thr Arg Asp
110 115 120

Phe Ala Leu Lys Gly Pro Asn Leu Arg Ile Gln Arg His Gly Lys Val
125 130 135

Phe Pro Asp Trp Thr His Lys Gly Met Glu Val Gly Thr Gly Tyr Asn
140 145 150

Arg Arg Trp Val Gln Leu Ser Gly Gly Pro Glu Phe Ser Phe Asp Leu
155 160 165

Leu Pro Glu Ala Arg Ala Ile Arg Val Thr Ile Ser Ser Gly Pro Glu
170 175 180 185

Val Ser Val Arg Leu Cys His Gln Trp Ala Leu Glu Cys Glu Glu Leu

190

195

200

Ser Ser Pro Tyr Asp Val Gln Lys Ile Val Ser Gly Gly His Thr Val
 205 210 215

Glu Leu Pro Tyr Glu Phe Leu Leu Pro Cys Leu Cys Ile Glu Ala Ser
 220 225 230

Tyr Leu Gln Glu Asp Thr Val Arg Arg Lys Lys Cys Pro Phe Gln Ser
 235 240 245

Trp Pro Glu Ala Tyr Gly Ser Asp Phe Trp Lys Ser Val His Phe Thr
 250 255 260 265

Asp Tyr Ser Gln His Thr Gln Met Val Met Ala Leu Thr Leu Arg Cys
 270 275 280

Pro Leu Lys Leu Glu Ala Ala Leu Cys Gln Arg His Asp Trp His Thr
 285 290 295

Leu Cys Lys Asp Leu Pro Asn Ala Thr Ala Arg Glu Ser Asp Gly Trp
 300 305 310

Tyr Val Leu Glu Lys Val Asp Leu His Pro Gln Leu Cys Phe Lys Val
 315 320 325

Gln Pro Trp Phe Ser Phe Gly Asn Ser Ser His Val Glu Cys Pro His
 330 335 340 345

Gln Thr Gly Ser Leu Thr Ser Trp Asn Val Ser Met Asp Thr Gln Ala
 350 355 360

Gln Gln Leu Ile Leu His Phe Ser Ser Arg Met His Ala Thr Phe Ser
 365 370 375

Ala Ala Trp Ser Leu Pro Gly Leu Gly Gln Asp Thr Leu Val Pro Pro
 380 385 390

Val Tyr Thr Val Ser Gln Val Trp Arg Ser Asp Val Gln Phe Ala Trp
 395 400 405

Lys His Leu Leu Cys Pro Asp Val Ser Tyr Arg His Leu Gly Leu Leu
 410 415 420 425

Ile Leu Ala Leu Leu Ala Leu Leu Thr Leu Leu Gly Val Val Leu Ala
 430 435 440

Leu Thr Cys Arg Arg Pro Gln Ser Gly Pro Gly Pro Ala Arg Pro Val
445 450 455

Leu Leu Leu His Ala Ala Asp Ser Glu Ala Gln Arg Arg Leu Val Gly
460 465 470

Ala Leu Ala Glu Leu Leu Arg Ala Ala Leu Gly Gly Gly Arg Asp Val
475 480 485

Ile Val Asp Leu Trp Glu Gly Arg His Val Ala Arg Val Gly Pro Leu
490 495 500 505

Pro Trp Leu Trp Ala Ala Arg Thr Arg Val Ala Arg Glu Gln Gly Thr
510 515 520

Val Leu Leu Leu Trp Ser Gly Ala Asp Leu Arg Pro Val Ser Gly Pro
525 530 535

Asp Pro Arg Ala Ala Pro Leu Leu Ala Leu Leu His Ala Ala Pro Arg
540 545 550

Pro Leu Leu Leu Leu Ala Tyr Phe Ser Arg Leu Cys Ala Lys Gly Asp
555 560 565

Ile Pro Pro Pro Leu Arg Ala Leu Pro Arg Tyr Arg Leu Leu Arg Asp
570 575 580 585

Leu Pro Arg Leu Leu Arg Ala Leu Asp Ala Arg Pro Phe Ala Glu Ala
590 595 600

Thr Ser Trp Gly Arg Leu Gly Ala Arg Gln Arg Arg Gln Ser Arg Leu
605 610 615

Glu Leu Cys Ser Arg Leu Glu Arg Glu Ala Ala Arg Leu Ala Asp Leu
620 625 630

Gly

<210> 13
<211> 808
<212> DNA
<213> Mus musculus

<220>
<221> CDS

<222> (78)..(806)
<223>

<220>
<221> mat_peptide
<222> (147)..()
<223>

<400> 13
cagctccggg ccaggccctg ctgccctctt gcagacagga aagacatggt ctctgcgccc 60
tgatcctaca gaagctc atg ggg agc ccc aga ctg gca gcc ttg ctc ctg 110
Met Gly Ser Pro Arg Leu Ala Ala Leu Leu Leu
-20 -15
tct ctc ccg cta ctg ctc atc ggc ctc gct gtg tct gct cgg gtt gcc 158
Ser Leu Pro Leu Leu Leu Ile Gly Leu Ala Val Ser Ala Arg Val Ala
-10 -5 -1 1
tgc ccc tgc ctg cgg agt tgg acc agc cac tgt ctc ctg gcc tac cgt 206
Cys Pro Cys Leu Arg Ser Trp Thr Ser His Cys Leu Leu Ala Tyr Arg
5 10 15 20
gtg gat aaa cgt ttt gct ggc ctt cag tgg ggc tgg ttc cct ctc ttg 254
Val Asp Lys Arg Phe Ala Gly Leu Gln Trp Gly Trp Phe Pro Leu Leu
25 30 35
gtg agg aaa tct aaa agt cct cct aaa ttt gaa gac tat tgg agg cac 302
Val Arg Lys Ser Lys Ser Pro Pro Lys Phe Glu Asp Tyr Trp Arg His
40 45 50
agg aca cca gca tcc ttc cag agg aag ctg cta ggc agc cct tcc ctg 350
Arg Thr Pro Ala Ser Phe Gln Arg Lys Leu Leu Gly Ser Pro Ser Leu
55 60 65
tct gag gaa agc cat cga att tcc atc ccc tcc tca gcc atc tcc cac 398
Ser Glu Glu Ser His Arg Ile Ser Ile Pro Ser Ser Ala Ile Ser His
70 75 80
aga ggc caa cgc acc aaa agg gcc cag cct tca gct gca gaa gga aga 446
Arg Gly Gln Arg Thr Lys Arg Ala Gln Pro Ser Ala Ala Glu Gly Arg
85 90 95 100
gaa cat ctc cct gaa gca ggg tca caa aag tgt gga gga cct gaa ttc 494
Glu His Leu Pro Glu Ala Gly Ser Gln Lys Cys Gly Gly Pro Glu Phe
105 110 115
tcc ttt gat ttg ctg ccc gag gtg cag gct gtt cgg gtg act att cct 542
Ser Phe Asp Leu Leu Pro Glu Val Gln Ala Val Arg Val Thr Ile Pro
120 125 130
gca ggc ccc aag gca cgt gtg cgc ctt tgt tat cag tgg gca ctg gaa 590
Ala Gly Pro Lys Ala Arg Val Arg Leu Cys Tyr Gln Trp Ala Leu Glu
135 140 145
tgt gaa gac ttg agt agc cct ttt gat acc cag aaa att gtg tct gga 638
Cys Glu Asp Leu Ser Ser Pro Phe Asp Thr Gln Lys Ile Val Ser Gly
150 155 160

ggg cac act gta gac ctg cct tat gaa ttc ctt ctg ccc tgc atg tgc 686
 Gly His Thr Val Asp Leu Pro Tyr Glu Phe Leu Leu Pro Cys Met Cys
 165 170 175 180

ata gag gcc tcc tac ctg caa gag gac act gtg agg cgc aaa agt gtc 734
 Ile Glu Ala Ser Tyr Leu Gln Glu Asp Thr Val Arg Arg Lys Ser Val
 185 190 195

cct tcc aga gct ggc ctg aag ctt atg gct cag act tct ggc agt caa 782
 Pro Ser Arg Ala Gly Leu Lys Leu Met Ala Gln Thr Ser Gly Ser Gln
 200 205 210

tac gct tca ctg act aca gcc agc ac 808
 Tyr Ala Ser Leu Thr Thr Ala Ser
 215 220

<210> 14
 <211> 243
 <212> PRT
 <213> Mus musculus

<400> 14

Met Gly Ser Pro Arg Leu Ala Ala Leu Leu Leu Ser Leu Pro Leu Leu
 -20 -15 -10

Leu Ile Gly Leu Ala Val Ser Ala Arg Val Ala Cys Pro Cys Leu Arg
 -5 -1 1 5

Ser Trp Thr Ser His Cys Leu Leu Ala Tyr Arg Val Asp Lys Arg Phe
 10 15 20 25

Ala Gly Leu Gln Trp Gly Trp Phe Pro Leu Leu Val Arg Lys Ser Lys
 30 35 40

Ser Pro Pro Lys Phe Glu Asp Tyr Trp Arg His Arg Thr Pro Ala Ser
 45 50 55

Phe Gln Arg Lys Leu Leu Gly Ser Pro Ser Leu Ser Glu Glu Ser His
 60 65 70

Arg Ile Ser Ile Pro Ser Ser Ala Ile Ser His Arg Gly Gln Arg Thr
 75 80 85

Lys Arg Ala Gln Pro Ser Ala Ala Glu Gly Arg Glu His Leu Pro Glu
 90 95 100 105

Ala Gly Ser Gln Lys Cys Gly Gly Pro Glu Phe Ser Phe Asp Leu Leu
 110 115 120

Pro Glu Val Gln Ala Val Arg Val Thr Ile Pro Ala Gly Pro Lys Ala

125

130

135

Arg Val Arg Leu Cys Tyr Gln Trp Ala Leu Glu Cys Glu Asp Leu Ser
 140 145 150

Ser Pro Phe Asp Thr Gln Lys Ile Val Ser Gly Gly His Thr Val Asp
 155 160 165

Leu Pro Tyr Glu Phe Leu Leu Pro Cys Met Cys Ile Glu Ala Ser Tyr
 170 175 180 185

Leu Gln Glu Asp Thr Val Arg Arg Lys Ser Val Pro Ser Arg Ala Gly
 190 195 200

Leu Lys Leu Met Ala Gln Thr Ser Gly Ser Gln Tyr Ala Ser Leu Thr
 205 210 215

Thr Ala Ser
 220

<210> 15
 <211> 2377
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (180)..(1874)
 <223>

<400> 15
 ttttgagcag aggccttcccta ggctccgtag aaatttgcat acagcttcca cttcctgctt 60
 cagagcctgt tcttctactt acctggggccc ggagaagggtg gagggagacg agaagccgcc 120
 gagagccgac taccctccgg gccagtcctg tctgtccgtg gtggatctaa gaaactaga 179
 atg aac cga agc att cct gtg gag gtt gat gaa tca gaa cca tac cca 227
 Met Asn Arg Ser Ile Pro Val Glu Val Asp Glu Ser Glu Pro Tyr Pro
 1 5 10 15
 agt cag ttg ctg aaa cca atc cca gaa tat tcc ccg gaa gag gaa tca 275
 Ser Gln Leu Leu Lys Pro Ile Pro Glu Tyr Ser Pro Glu Glu Glu Ser
 20 25 30
 gaa cca cct gct cca aat ata agg aac atg gca ccc aac agc ttg tct 323
 Glu Pro Pro Ala Pro Asn Ile Arg Asn Met Ala Pro Asn Ser Leu Ser
 35 40 45
 gca ccc aca atg ctt cac aat tcc tcc gga gac ttt tct caa gct cac 371
 Ala Pro Thr Met Leu His Asn Ser Ser Gly Asp Phe Ser Gln Ala His
 50 55 60

tca acc ctg aaa ctt gca aat cac cag cgg cct gta tcc cgg cag gtc Ser Thr Leu Lys Leu Ala Asn His Gln Arg Pro Val Ser Arg Gln Val 65 70 75 80	419
acc tgc ctg cgc act caa gtt ctg gag gac agt gaa gac agt ttc tgc Thr Cys Leu Arg Thr Gln Val Leu Glu Asp Ser Glu Asp Ser Phe Cys 85 90 95	467
agg aga cac cca ggc ctg ggc aaa gct ttc cct tct ggg tgc tct gca Arg Arg His Pro Gly Leu Gly Lys Ala Phe Pro Ser Gly Cys Ser Ala 100 105 110	515
gtc agc gag cct gcg tct gag tct gtg gtt gga gcc ctc cct gca gag Val Ser Glu Pro Ala Ser Glu Ser Val Val Gly Ala Leu Pro Ala Glu 115 120 125	563
cat cag ttt tca ttt atg gaa aaa cgt aat caa tgg ctg gta tct cag His Gln Phe Ser Phe Met Glu Lys Arg Asn Gln Trp Leu Val Ser Gln 130 135 140	611
ctt tca gcg gct tct cct gac act ggc cat gac tca gac aaa tca gac Leu Ser Ala Ala Ser Pro Asp Thr Gly His Asp Ser Asp Lys Ser Asp 145 150 155 160	659
caa agt tta cct aat gcc tca gca gac tcc ttg ggc ggt agc cag gag Gln Ser Leu Pro Asn Ala Ser Ala Asp Ser Leu Gly Gly Ser Gln Glu 165 170 175	707
atg gtg caa cgg ccc cag cct cac agg aac cga gca ggc ctg gat ctg Met Val Gln Arg Pro Gln Pro His Arg Asn Arg Ala Gly Leu Asp Leu 180 185 190	755
cca acc ata gac acg gga tat gat tcc cag ccc cag gat gtc ctg ggc Pro Thr Ile Asp Thr Gly Tyr Asp Ser Gln Pro Gln Asp Val Leu Gly 195 200 205	803
atc agg cag ctg gaa agg ccc ctg ccc ctc acc tcc gtg tgt tac ccc Ile Arg Gln Leu Glu Arg Pro Leu Pro Leu Thr Ser Val Cys Tyr Pro 210 215 220	851
cag gac ctc ccc aga cct ctc agg tcc agg gag ttc cct cag ttt gaa Gln Asp Leu Pro Arg Pro Leu Arg Ser Arg Glu Phe Pro Gln Phe Glu 225 230 235 240	899
cct cag agg tat cca gca tgt gca cag atg ctg cct ccc aat ctt tcc Pro Gln Arg Tyr Pro Ala Cys Ala Gln Met Leu Pro Pro Asn Leu Ser 245 250 255	947
cca cat gct cca tgg aac tat cat tac cat tgt cct gga agt ccc gat Pro His Ala Pro Trp Asn Tyr His Tyr His Cys Pro Gly Ser Pro Asp 260 265 270	995
cac cag gtg cca tat ggc cat gac tac cct cga gca gcc tac cag caa His Gln Val Pro Tyr Gly His Asp Tyr Pro Arg Ala Ala Tyr Gln Gln 275 280 285	1043
gtg atc cag ccg gct ctg cct ggg cag ccc ctg cct gga gcc agt gtg Val Ile Gln Pro Ala Leu Pro Gly Gln Pro Leu Pro Gly Ala Ser Val 290 295 300	1091
aga ggc ctg cac cct gtg cag aag gtt atc ctg aat tat ccc agc ccc	1139

Arg Gly Leu His Pro Val Gln Lys Val Ile Leu Asn Tyr Pro Ser Pro	
305 310 315 320	
tgg gac caa gaa gag agg ccc gca cag aga gac tgc tcc ttt ccg ggg	1187
Trp Asp Gln Glu Glu Arg Pro Ala Gln Arg Asp Cys Ser Phe Pro Gly	
325 330 335	
ctt cca agg cac cag gac cag cca cat cac cag cca cct aat aga gct	1235
Leu Pro Arg His Gln Asp Gln Pro His His Gln Pro Pro Asn Arg Ala	
340 345 350	
ggg gct cct ggg gag tcc ttg gag tgc cct gca gag ctg aga cca cag	1283
Gly Ala Pro Gly Glu Ser Leu Glu Cys Pro Ala Glu Leu Arg Pro Gln	
355 360 365	
gtt ccc cag cct ccg tcc cca gct gct gtg cct aga ccc cct agc aac	1331
Val Pro Gln Pro Pro Ser Pro Ala Ala Val Pro Arg Pro Pro Ser Asn	
370 375 380	
cct cca gcc aga gga act cta aaa aca agc aat ttg cca gaa gaa ttg	1379
Pro Pro Ala Arg Gly Thr Leu Lys Thr Ser Asn Leu Pro Glu Glu Leu	
385 390 395 400	
cgg aaa gtc ttt atc act tat tgc atg gac aca gct atg gag gtg gtg	1427
Arg Lys Val Phe Ile Thr Tyr Ser Met Asp Thr Ala Met Glu Val Val	
405 410 415	
aaa ttc gtg aac ttt ttg ttg gta aat ggc ttc caa act gca att gac	1475
Lys Phe Val Asn Phe Leu Leu Val Asn Gly Phe Gln Thr Ala Ile Asp	
420 425 430	
ata ttt gag gat aga atc cga ggc att gat atc att aaa tgg atg gag	1523
Ile Phe Glu Asp Arg Ile Arg Gly Ile Asp Ile Ile Lys Trp Met Glu	
435 440 445	
cgc tac ctt agg gat aag acc gtg atg ata atc gta gca atc agc ccc	1571
Arg Tyr Leu Arg Asp Lys Thr Val Met Ile Ile Val Ala Ile Ser Pro	
450 455 460	
aaa tac aaa cag gac gtg gaa ggc gct gag tgc cag ctg gac gag gat	1619
Lys Tyr Lys Gln Asp Val Glu Gly Ala Glu Ser Gln Leu Asp Glu Asp	
465 470 475 480	
gag cat ggc tta cat act aag tac att cat cga atg atg cag att gag	1667
Glu His Gly Leu His Thr Lys Tyr Ile His Arg Met Met Gln Ile Glu	
485 490 495	
ttc ata aaa caa gga agc atg aat ttc aga ttc atc cct gtg ctc ttc	1715
Phe Ile Lys Gln Gly Ser Met Asn Phe Arg Phe Ile Pro Val Leu Phe	
500 505 510	
cca aat gct aag aag gag cat gtg ccc acc tgg ctt cag aac act cat	1763
Pro Asn Ala Lys Lys Glu His Val Pro Thr Trp Leu Gln Asn Thr His	
515 520 525	
gtc tac agc tgg ccc aag aat aaa aaa aac atc ctg ctg cgg ctg ctg	1811
Val Tyr Ser Trp Pro Lys Asn Lys Lys Asn Ile Leu Leu Arg Leu Leu	
530 535 540	
aga gag gaa gag tat gtg gct cct cca cgg ggg cct ctg ccc acc ctt	1859
Arg Glu Glu Glu Tyr Val Ala Pro Pro Arg Gly Pro Leu Pro Thr Leu	

545	550	555	560	
cag gtg gtt ccc ttg tgacaccgtt catccccaga tcaactgaggc caggccatgt				1914
Gln Val Val Pro Leu				
565				
ttggggcctt gttctgacag cattctggct gaggctggtc ggtagcactc ctggctggtt				1974
tttttctgtt cctccccgag aggccctctg gccccagga aacctgttgt gcagagctct				2034
tccccggaga cctccacaca ccctggcttt gaagtggagt ctgtgactgc tctgcattct				2094
ctgcttttaa aaaaaccatt gcaggtgccca gtgtcccata tgttcctcct gacagtttga				2154
tgtgtccatt ctgggcctct cagtgccttag caagtagata atgtaaggga tgtggcagca				2214
aatggaaatg actacaaaca ctctcctatc aatcacttca ggctactttt atgagtttagc				2274
cagatgcttg tgtatcctca gaccaaactg attcatgtac aaataataaa atgtttactc				2334
ttttgtaaaa aaaaaaaaaa aaaaaaaaaag aaaaaaaaaa aaa				2377

<210> 16
 <211> 565
 <212> PRT
 <213> Homo sapiens

<400> 16

Met	Asn	Arg	Ser	Ile	Pro	Val	Glu	Val	Asp	Glu	Ser	Glu	Pro	Tyr	Pro
1				5					10					15	

Ser	Gln	Leu	Leu	Lys	Pro	Ile	Pro	Glu	Tyr	Ser	Pro	Glu	Glu	Glu	Ser
		20						25					30		

Glu	Pro	Pro	Ala	Pro	Asn	Ile	Arg	Asn	Met	Ala	Pro	Asn	Ser	Leu	Ser
		35					40					45			

Ala	Pro	Thr	Met	Leu	His	Asn	Ser	Ser	Gly	Asp	Phe	Ser	Gln	Ala	His
		50				55					60				

Ser	Thr	Leu	Lys	Leu	Ala	Asn	His	Gln	Arg	Pro	Val	Ser	Arg	Gln	Val
65					70					75				80	

Thr	Cys	Leu	Arg	Thr	Gln	Val	Leu	Glu	Asp	Ser	Glu	Asp	Ser	Phe	Cys
			85						90					95	

Arg	Arg	His	Pro	Gly	Leu	Gly	Lys	Ala	Phe	Pro	Ser	Gly	Cys	Ser	Ala
			100					105					110		

Val	Ser	Glu	Pro	Ala	Ser	Glu	Ser	Val	Val	Gly	Ala	Leu	Pro	Ala	Glu
		115						120				125			

His Gln Phe Ser Phe Met Glu Lys Arg Asn Gln Trp Leu Val Ser Gln
130 135 140

Leu Ser Ala Ala Ser Pro Asp Thr Gly His Asp Ser Asp Lys Ser Asp
145 150 155 160

Gln Ser Leu Pro Asn Ala Ser Ala Asp Ser Leu Gly Gly Ser Gln Glu
165 170 175

Met Val Gln Arg Pro Gln Pro His Arg Asn Arg Ala Gly Leu Asp Leu
180 185 190

Pro Thr Ile Asp Thr Gly Tyr Asp Ser Gln Pro Gln Asp Val Leu Gly
195 200 205

Ile Arg Gln Leu Glu Arg Pro Leu Pro Leu Thr Ser Val Cys Tyr Pro
210 215 220

Gln Asp Leu Pro Arg Pro Leu Arg Ser Arg Glu Phe Pro Gln Phe Glu
225 230 235 240

Pro Gln Arg Tyr Pro Ala Cys Ala Gln Met Leu Pro Pro Asn Leu Ser
245 250 255

Pro His Ala Pro Trp Asn Tyr His Tyr His Cys Pro Gly Ser Pro Asp
260 265 270

His Gln Val Pro Tyr Gly His Asp Tyr Pro Arg Ala Ala Tyr Gln Gln
275 280 285

Val Ile Gln Pro Ala Leu Pro Gly Gln Pro Leu Pro Gly Ala Ser Val
290 295 300

Arg Gly Leu His Pro Val Gln Lys Val Ile Leu Asn Tyr Pro Ser Pro
305 310 315 320

Trp Asp Gln Glu Glu Arg Pro Ala Gln Arg Asp Cys Ser Phe Pro Gly
325 330 335

Leu Pro Arg His Gln Asp Gln Pro His His Gln Pro Pro Asn Arg Ala
340 345 350

Gly Ala Pro Gly Glu Ser Leu Glu Cys Pro Ala Glu Leu Arg Pro Gln
355 360 365

Val Pro Gln Pro Pro Ser Pro Ala Ala Val Pro Arg Pro Pro Ser Asn
370 375 380

Pro Pro Ala Arg Gly Thr Leu Lys Thr Ser Asn Leu Pro Glu Glu Leu
385 390 395 400

Arg Lys Val Phe Ile Thr Tyr Ser Met Asp Thr Ala Met Glu Val Val
405 410 415

Lys Phe Val Asn Phe Leu Leu Val Asn Gly Phe Gln Thr Ala Ile Asp
420 425 430

Ile Phe Glu Asp Arg Ile Arg Gly Ile Asp Ile Ile Lys Trp Met Glu
435 440 445

Arg Tyr Leu Arg Asp Lys Thr Val Met Ile Ile Val Ala Ile Ser Pro
450 455 460

Lys Tyr Lys Gln Asp Val Glu Gly Ala Glu Ser Gln Leu Asp Glu Asp
465 470 475 480

Glu His Gly Leu His Thr Lys Tyr Ile His Arg Met Met Gln Ile Glu
485 490 495

Phe Ile Lys Gln Gly Ser Met Asn Phe Arg Phe Ile Pro Val Leu Phe
500 505 510

Pro Asn Ala Lys Lys Glu His Val Pro Thr Trp Leu Gln Asn Thr His
515 520 525

Val Tyr Ser Trp Pro Lys Asn Lys Lys Asn Ile Leu Leu Arg Leu Leu
530 535 540

Arg Glu Glu Glu Tyr Val Ala Pro Pro Arg Gly Pro Leu Pro Thr Leu
545 550 555 560

Gln Val Val Pro Leu
565

<210> 17
<211> 1323
<212> DNA
<213> Mus musculus

<220>
<221> CDS
<222> (1)..(1026)
<223>

<400> 17

cag gac ctc cct ggg cct ctg agg tcc agg gaa ttg cca cct cag ttt	48
Gln Asp Leu Pro Gly Pro Leu Arg Ser Arg Glu Leu Pro Pro Gln Phe	
1 5 10 15	
gaa ctt gag agg tat cca atg aac gcc cag ctg ctg ccg ccc cat cct	96
Glu Leu Glu Arg Tyr Pro Met Asn Ala Gln Leu Leu Pro Pro His Pro	
20 25 30	
tcc cca cag gcc cca tgg aac tgt cag tac tac tgc ccc gga ggg ccc	144
Ser Pro Gln Ala Pro Trp Asn Cys Gln Tyr Tyr Cys Pro Gly Gly Pro	
35 40 45	
tac cac cac cag gtg cca cac ggc cat ggc tac cct cca gca gca gcc	192
Tyr His His Gln Val Pro His Gly His Gly Tyr Pro Pro Ala Ala Ala	
50 55 60	
tac cag caa gta ctc cag cct gct ctg cct ggg cag gtc ctt cct ggg	240
Tyr Gln Gln Val Leu Gln Pro Ala Leu Pro Gly Gln Val Leu Pro Gly	
65 70 75 80	
gca agg gca aga ggc cca cgc cct gtg cag aag gtc atc ctg aat gac	288
Ala Arg Ala Arg Gly Pro Arg Pro Val Gln Lys Val Ile Leu Asn Asp	
85 90 95	
tcc agc ccc caa gac caa gaa gag aga cct gca cag aga gac ttc tct	336
Ser Ser Pro Gln Asp Gln Glu Glu Arg Pro Ala Gln Arg Asp Phe Ser	
100 105 110	
ttc ccg agg ctc ccg agg gac cag ctc tac cgc cca cca tct aat gga	384
Phe Pro Arg Leu Pro Arg Asp Gln Leu Tyr Arg Pro Pro Ser Asn Gly	
115 120 125	
gtg gaa gcc cct gag gag tcc ttg gac ctt cct gca gag ctg aga cca	432
Val Glu Ala Pro Glu Glu Ser Leu Asp Leu Pro Ala Glu Leu Arg Pro	
130 135 140	
cat ggt ccc cag gct cca tcc cta gct gcc gtg cct aga ccc cct agc	480
His Gly Pro Gln Ala Pro Ser Leu Ala Ala Val Pro Arg Pro Pro Ser	
145 150 155 160	
aac ccc tta gcc cga gga act cta aga acc agc aat ttg cca gaa gaa	528
Asn Pro Leu Ala Arg Gly Thr Leu Arg Thr Ser Asn Leu Pro Glu Glu	
165 170 175	
tta cgg aaa gtc ttt atc act tat tct atg gac aca gcc atg gag gtg	576
Leu Arg Lys Val Phe Ile Thr Tyr Ser Met Asp Thr Ala Met Glu Val	
180 185 190	
gtg aaa ttt gtg aac ttt ctg ttg gtg aac ggc ttc caa act gcg att	624
Val Lys Phe Val Asn Phe Leu Leu Val Asn Gly Phe Gln Thr Ala Ile	
195 200 205	
gac ata ttt gag gat aga atc cgg ggt att gat atc att aaa tgg atg	672
Asp Ile Phe Glu Asp Arg Ile Arg Gly Ile Asp Ile Ile Lys Trp Met	
210 215 220	
gag cgc tat ctt cga gat aag aca gtg atg ata atc gta gca atc agc	720
Glu Arg Tyr Leu Arg Asp Lys Thr Val Met Ile Ile Val Ala Ile Ser	

225	230	235	240	
ccc aaa tac aaa cag gat gtg gaa ggc gct gag tcg cag ctg gac gag				768
Pro Lys Tyr Lys Gln Asp Val Glu Gly Ala Glu Ser Gln Leu Asp Glu				
245	250	255		
gac gag cat ggc tta cat act aag tac att cat cgg atg atg cag att				816
Asp Glu His Gly Leu His Thr Lys Tyr Ile His Arg Met Met Gln Ile				
260	265	270		
gag ttc ata agt cag gga agc atg aac ttc aga ttc atc cct gtg ctc				864
Glu Phe Ile Ser Gln Gly Ser Met Asn Phe Arg Phe Ile Pro Val Leu				
275	280	285		
ttc cca aat gcc aag aag gag cat gtg ccg acc tgg ctt cag aac act				912
Phe Pro Asn Ala Lys Lys Glu His Val Pro Thr Trp Leu Gln Asn Thr				
290	295	300		
cat gtt tac agc tgg ccc aag aat aag aaa aac atc ctg ctg cgg ctg				960
His Val Tyr Ser Trp Pro Lys Asn Lys Lys Asn Ile Leu Leu Arg Leu				
305	310	315	320	
ctc agg gag gaa gag tat gtg gct cct ccc cga ggc cct ctg ccc acc				1008
Leu Arg Glu Glu Glu Tyr Val Ala Pro Pro Arg Gly Pro Leu Pro Thr				
325	330	335		
ctt cag gtg gta ccc ttg tgacgatggc cactccagct cagtgccagc				1056
Leu Gln Val Val Pro Leu				
340				
ctgtttctcac agcattcttc tagcggagct ggctggtggc acccaggccc tggaacacct				1116
cttctacaga gtctctgtc tcttgagtct gagttgtcct cgctgggctt ccagagcttc				1176
agtgcctgga tgctgcaggt gacagaaaca aacatctatg accacaaaaa ctctcatcac				1236
ttcagctact tttatgagtc ggtcagatgc tctgtgtcct tagaccagtc taaatcatgc				1296
tcaaataata aaatgattat tctttgt				1323
<210> 18				
<211> 342				
<212> PRT				
<213> Mus musculus				
<400> 18				
Gln Asp Leu Pro Gly Pro Leu Arg Ser Arg Glu Leu Pro Pro Gln Phe				
1 5 10 15				
Glu Leu Glu Arg Tyr Pro Met Asn Ala Gln Leu Leu Pro Pro His Pro				
20 25 30				
Ser Pro Gln Ala Pro Trp Asn Cys Gln Tyr Tyr Cys Pro Gly Gly Pro				
35 40 45				
Tyr His His Gln Val Pro His Gly His Gly Tyr Pro Pro Ala Ala Ala				

50

55

60

Tyr Gln Gln Val Leu Gln Pro Ala Leu Pro Gly Gln Val Leu Pro Gly
65 70 75 80

Ala Arg Ala Arg Gly Pro Arg Pro Val Gln Lys Val Ile Leu Asn Asp
85 90 95

Ser Ser Pro Gln Asp Gln Glu Glu Arg Pro Ala Gln Arg Asp Phe Ser
100 105 110

Phe Pro Arg Leu Pro Arg Asp Gln Leu Tyr Arg Pro Pro Ser Asn Gly
115 120 125

Val Glu Ala Pro Glu Glu Ser Leu Asp Leu Pro Ala Glu Leu Arg Pro
130 135 140

His Gly Pro Gln Ala Pro Ser Leu Ala Ala Val Pro Arg Pro Pro Ser
145 150 155 160

Asn Pro Leu Ala Arg Gly Thr Leu Arg Thr Ser Asn Leu Pro Glu Glu
165 170 175

Leu Arg Lys Val Phe Ile Thr Tyr Ser Met Asp Thr Ala Met Glu Val
180 185 190

Val Lys Phe Val Asn Phe Leu Leu Val Asn Gly Phe Gln Thr Ala Ile
195 200 205

Asp Ile Phe Glu Asp Arg Ile Arg Gly Ile Asp Ile Ile Lys Trp Met
210 215 220

Glu Arg Tyr Leu Arg Asp Lys Thr Val Met Ile Ile Val Ala Ile Ser
225 230 235 240

Pro Lys Tyr Lys Gln Asp Val Glu Gly Ala Glu Ser Gln Leu Asp Glu
245 250 255

Asp Glu His Gly Leu His Thr Lys Tyr Ile His Arg Met Met Gln Ile
260 265 270

Glu Phe Ile Ser Gln Gly Ser Met Asn Phe Arg Phe Ile Pro Val Leu
275 280 285

Phe Pro Asn Ala Lys Lys Glu His Val Pro Thr Trp Leu Gln Asn Thr
290 295 300

His Val Tyr Ser Trp Pro Lys Asn Lys Lys Asn Ile Leu Leu Arg Leu
305 310 315 320

Leu Arg Glu Glu Glu Tyr Val Ala Pro Pro Arg Gly Pro Leu Pro Thr
325 330 335

Leu Gln Val Val Pro Leu
340

<210> 19
<211> 207
<212> PRT
<213> Homo sapiens

<400> 19

Arg Lys Val Trp Ile Ile Tyr Ser Ala Asp His Pro Leu Tyr Val Asp
1 5 10 15

Val Val Leu Lys Phe Ala Gln Phe Leu Leu Thr Ala Cys Gly Thr Glu
20 25 30

Val Ala Leu Asp Leu Leu Glu Glu Gln Ala Ile Ser Glu Ala Gly Val
35 40 45

Met Thr Trp Val Gly Arg Gln Lys Gln Glu Met Val Glu Ser Asn Ser
50 55 60

Lys Ile Ile Val Leu Cys Ser Arg Gly Thr Arg Ala Lys Trp Gln Ala
65 70 75 80

Leu Leu Gly Arg Gly Ala Pro Val Arg Leu Arg Cys Asp His Gly Lys
85 90 95

Pro Val Gly Asp Leu Phe Thr Ala Ala Met Asn Met Ile Leu Pro Asp
100 105 110

Phe Lys Arg Pro Ala Cys Phe Gly Thr Tyr Val Val Cys Tyr Phe Ser
115 120 125

Glu Val Ser Cys Asp Gly Asp Val Pro Asp Leu Phe Gly Ala Ala Pro
130 135 140

Arg Tyr Pro Leu Met Asp Arg Phe Glu Glu Val Tyr Phe Arg Ile Gln
145 150 155 160

Asp Leu Glu Met Phe Gln Pro Gly Arg Met His Arg Val Gly Glu Leu
165 170 175

Ser Gly Asp Asn Tyr Leu Arg Ser Pro Gly Gly Arg Gln Leu Arg Ala
180 185 190

Ala Leu Asp Arg Phe Arg Asp Trp Gln Val Arg Cys Pro Asp Trp
195 200 205

<210> 20
<211> 208
<212> PRT
<213> Mus musculus

<400> 20

Arg Lys Val Trp Ile Val Tyr Ser Ala Asp His Pro Leu Tyr Val Glu
1 5 10 15

Val Val Leu Lys Phe Ala Gln Phe Leu Ile Thr Ala Cys Gly Thr Glu
20 25 30

Val Ala Leu Asp Leu Leu Glu Glu Gln Val Ile Ser Glu Val Gly Val
35 40 45

Met Thr Trp Val Ser Arg Gln Lys Gln Glu Met Val Glu Ser Asn Ser
50 55 60

Lys Ile Ile Ile Leu Cys Ser Arg Gly Thr Gln Ala Lys Trp Lys Ala
65 70 75 80

Ile Leu Gly Trp Ala Glu Pro Ala Val Gln Leu Arg Cys Asp His Trp
85 90 95

Lys Pro Ala Gly Asp Leu Phe Thr Ala Ala Met Asn Met Ile Leu Pro
100 105 110

Asp Phe Lys Arg Pro Ala Cys Phe Gly Thr Tyr Val Val Cys Tyr Phe
115 120 125

Ser Gly Ile Cys Ser Glu Arg Asp Val Pro Asp Leu Phe Asn Ile Thr
130 135 140

Ser Arg Tyr Pro Leu Met Asp Arg Phe Glu Glu Val Tyr Phe Arg Ile
145 150 155 160

Gln Asp Leu Glu Met Phe Glu Pro Gly Arg Met His His Val Arg Glu
165 170 175

Leu Thr Gly Asp Asn Tyr Leu Gln Ser Pro Ser Gly Arg Gln Leu Lys
180 185 190

Glu Ala Val Leu Arg Phe Gln Glu Trp Gln Thr Gln Cys Pro Asp Trp
195 200 205

<210> 21
<211> 190
<212> PRT
<213> Caenorhabditis elegans

<400> 21

Val Lys Val Met Ile Val Tyr Ala Asp Asp Asn Asp Leu His Thr Asp
1 5 10 15

Cys Val Lys Lys Leu Val Glu Asn Leu Arg Asn Cys Ala Ser Cys Asp
20 25 30

Pro Val Phe Asp Leu Glu Lys Leu Ile Thr Ala Glu Ile Val Pro Ser
35 40 45

Arg Trp Leu Val Asp Gln Ile Ser Ser Leu Lys Lys Phe Ile Ile Val
50 55 60

Val Ser Asp Cys Ala Glu Lys Ile Leu Asp Thr Glu Ala Ser Glu Thr
65 70 75 80

His Gln Leu Val Gln Ala Arg Pro Phe Ala Asp Leu Phe Gly Pro Ala
85 90 95

Met Glu Met Ile Ile Arg Asp Ala Thr His Asn Phe Pro Glu Ala Arg
100 105 110

Lys Lys Tyr Ala Val Val Arg Phe Asn Tyr Ser Pro His Val Pro Pro
115 120 125

Asn Leu Ala Ile Leu Asn Leu Pro Thr Phe Ile Pro Glu Gln Phe Ala
130 135 140

Gln Leu Thr Ala Phe Leu His Asn Val Glu His Thr Glu Arg Ala Asn
145 150 155 160

Val Thr Gln Asn Ile Ser Glu Ala Gln Ile His Glu Trp Asn Leu Cys
165 170 175

Ala Ser Arg Met Met Ser Phe Phe Val Arg Asn Pro Asn Trp
180 185 190

<210> 22
<211> 178
<212> PRT
<213> Caenorhabditis elegans

<400> 22

Phe Lys Val Met Leu Val Cys Pro Glu Val Ser Gly Arg Asp Glu Asp
1 5 10 15

Phe Met Met Arg Ile Ala Asp Ala Leu Lys Lys Ser Asn Asn Lys Val
20 25 30

Val Cys Asp Arg Trp Phe Glu Asp Ser Lys Asn Ala Glu Glu Asn Met
35 40 45

Leu His Trp Val Tyr Glu Gln Thr Lys Ile Ala Glu Lys Ile Ile Val
50 55 60

Phe His Ser Ala Tyr Tyr His Pro Arg Cys Gly Ile Tyr Asp Val Ile
65 70 75 80

Asn Asn Phe Phe Pro Cys Thr Asp Pro Arg Leu Ala His Ile Ala Leu
85 90 95

Thr Pro Glu Ala Gln Arg Ser Val Pro Lys Glu Val Glu Tyr Val Leu
100 105 110

Pro Arg Asp Gln Lys Leu Leu Glu Asp Ala Phe Asp Ile Thr Ile Ala
115 120 125

Asp Pro Leu Val Ile Asp Ile Pro Ile Glu Asp Val Ala Ile Pro Glu
130 135 140

Asn Val Pro Ile His His Glu Ser Cys Asp Ser Ile Asp Ser Arg Asn
145 150 155 160

Asn Ser Lys Thr His Ser Thr Asp Ser Gly Val Ser Ser Leu Ser Ser
165 170 175

Asn Ser